



#6

SEQUENCE LISTING

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Tang, Liang  
Heska Corporation

<120> COMPOSITIONS AND METHODS RELATED TO CANINE IgG AND  
CANINE IL-13 RECEPTORS

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<141> 2001-04-09

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<170> PatentIn Ver. 2.1

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 Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe  
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acc ttc agt tgc tac tac atg cat tgg atc cgc cag gct cca ggg aag 255  
 Thr Phe Ser Ser Tyr Tyr Met His Trp Ile Arg Gln Ala Pro Gly Lys  
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 Gly Leu Gln Arg Val Ala His Ile Arg Gly Asp Gly Arg Thr Thr His  
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Tyr Ala Asp Ala Met Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala	
80 85 90	
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Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Thr Val Glu Asp Thr	
95 100 105 110	
gct att tat tac tgt gta aag gac ata tac tat ggg gtc ggg gac tat	447
Ala Ile Tyr Tyr Cys Val Lys Asp Ile Tyr Tyr Gly Val Gly Asp Tyr	
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Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Thr Ala	
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Pro Ser Val Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser	
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Thr Val Ala Leu Ala Cys Leu Val Ser Gly Tyr Phe Pro Glu Pro Val	
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Pro Ser Val Leu Gln Ser Ser Gly Leu His Ser Leu Ser Ser Met Val	
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Val His Pro Ala Ser Asn Thr Lys Val Asp Lys Pro Val Phe Asn Glu	
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Cys Arg Cys Thr Asp Thr Pro Pro Cys Pro Val Pro Glu Pro Leu Gly	
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Gly Pro Ser Val Leu Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg	
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Ile Thr Arg Thr Pro Glu Val Thr Cys Val Val Leu Asp Leu Gly Arg	
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Glu Asp Pro Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val	
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His Thr Ala Lys Thr Gln Ser Arg Glu Gln Gln Phe Asn Gly Thr Tyr	
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Arg Val Val Ser Val Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly	
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Lys Glu Phe Lys Cys Arg Val Asn His Ile Asp Leu Pro Ser Pro Ile	
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Glu Arg Thr Ile Ser Lys Ala Arg Gly Arg Ala His Lys Pro Ser Val	
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Tyr Val Leu Pro Pro Ser Pro Lys Glu Leu Ser Ser Ser Asp Thr Val	
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Ser Ile Thr Cys Leu Ile Lys Asp Phe Tyr Pro Pro Asp Ile Asp Val	
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Glu Trp Gln Ser Asn Gly Gln Gln Glu Pro Glu Arg Lys His Arg Met	
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 acc ccg ccc cag ctg gac gag gac ggg tcc tac ttc ctg tac agc aag	1359
Thr Pro Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys	
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Leu Ser Val Asp Lys Ser Arg Trp Gln Gln Gly Asp Pro Phe Thr Cys	
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 Ser His Ser Pro Gly Lys  
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Pro Gly Gly Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe  
 35 40 45

Ser Ser Tyr Tyr Met His Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu  
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Gln Arg Val Ala His Ile Arg Gly Asp Gly Arg Thr Thr His Tyr Ala  
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Asp Ala Met Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn  
 85 90 95

Thr Leu Tyr Leu Gln Met Asn Ser Leu Thr Val Glu Asp Thr Ala Ile  
 100 105 110

Tyr Tyr Cys Val Lys Asp Ile Tyr Tyr Gly Val Gly Asp Tyr Trp Gly  
 115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Thr Ala Pro Ser  
 130 135 140

Val Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser Thr Val  
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Cys	Thr	Asp	Thr	Pro	Pro	Cys	Pro	Val	Pro	Glu	Pro	Leu	Gly	Gly	Pro		
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Ser	Val	Leu	Ile	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Ile	Leu	Arg	Ile	Thr		
		260						265					270				
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Pro	Glu	Val	Gln	Ile	Ser	Trp	Phe	Val	Asp	Gly	Lys	Glu	Val	His	Thr		
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Leu	Pro	Pro	Ser	Pro	Lys	Glu	Leu	Ser	Ser	Ser	Asp	Thr	Val	Ser	Ile		
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Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser  
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Val Asp Lys Ser Arg Trp Gln Gln Gly Asp Pro Phe Thr Cys Ala Val  
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 cgggctcctg ctgtccattg ctctgccact ccacatcaat gtcaggtggg tagaagtctt 420  
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gag gtg caa ctg gtg gag tct ggg gga gac ctg gtg aag cct ggg ggg      152
Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys Pro Gly Gly
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tcc ttg aga ctg tcc tgt gtg gcc tct gga ttc acc ttc agt gac tat      200
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Asp Tyr
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ggc atg agt tgg gtc cgt cag tct cca ggg aag ggg ctg cag tgg gtc      248
Gly Met Ser Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Gln Trp Val
                      55                      60                      65

gca gct gtt agc aat cgt gga gat act tac tac gca gac gct gtg aag      296
Ala Ala Val Ser Asn Arg Gly Asp Thr Tyr Tyr Ala Asp Ala Val Lys
      70                      75                      80

ggc cga ttc acc atc tcc aga gac aac gcc aag aac acg ctg tat ctc      344
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu
      85                      90                      95

cag atg agc agc ctg aaa gcc gag gac acg gca atc tat cac tgt gtg      392
Gln Met Ser Ser Leu Lys Ala Glu Asp Thr Ala Ile Tyr His Cys Val
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acg gga gta tgg ccg cga cat tat tat ggt atg gac cac tgg ggc aat      440
Thr Gly Val Trp Pro Arg His Tyr Tyr Gly Met Asp His Trp Gly Asn
                      120                      125                      130

ggc acc tca ctc ttc gtg tcc tca gcc tcc acc acg gcc ccc tcg gtt      488
Gly Thr Ser Leu Phe Val Ser Ser Ala Ser Thr Thr Ala Pro Ser Val
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ttc cca ctg gcc ccc agc tgc ggg tcc act tcc ggc tcc acg gtg gcc      536
Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser Thr Val Ala
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Trp Asn Ser Gly Ser Leu Thr Ser Gly Val His Thr Phe Pro Ser Val	
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ctg cag tcc tca ggg ctc tac tcc ctc agc agc acg gtg aca gtg ccc	680
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Thr Val Thr Val Pro	
200 205 210	
tcc agc agg tgg ccc agc gag acc ttc acc tgc aac gtg gtc cac ccg	728
Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val Val His Pro	
215 220 225	
gcc agc aac act aaa gta gac aag cca gtg ccc aaa gag tcc acc tgc	776
Ala Ser Asn Thr Lys Val Asp Lys Pro Val Pro Lys Glu Ser Thr Cys	
230 235 240	
aag tgt ata tcc cca tgc cca gtc cct gaa tca ctg gga ggg cct tgc	824
Lys Cys Ile Ser Pro Cys Pro Val Pro Glu Ser Leu Gly Gly Pro Ser	
245 250 255	
gtc ttc atc ttt ccc ccg aaa ccc aag gac atc ctc agg att acc cga	872
Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg Ile Thr Arg	
260 265 270 275	
aca ccc gag atc acc tgt gtg gtg tta gat ctg ggc cgt gag gac cct	920
Thr Pro Glu Ile Thr Cys Val Val Leu Asp Leu Gly Arg Glu Asp Pro	
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gag gtg cag atc agc tgg ttc gtg gat ggt aag gag gtg cac aca gcc	968
Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val His Thr Ala	
295 300 305	
aag acg cag cct cgt gag cag cag ttc aac agc acc tac cgt gtg gtc	1016
Lys Thr Gln Pro Arg Glu Gln Gln Phe Asn Ser Thr Tyr Arg Val Val	
310 315 320	
agc gtc ctc ccc att gag cac cag gac tgg ctc acc gga aag gag ttc	1064
Ser Val Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly Lys Glu Phe	
325 330 335	
aag tgc aga gtc aac cac ata ggc ctc ccg tcc ccc atc gag agg act	1112
Lys Cys Arg Val Asn His Ile Gly Leu Pro Ser Pro Ile Glu Arg Thr	
340 345 350 355	

atc tcc aaa gcc aga ggg caa gcc cat cag ccc agt gtg tat gtc ctg 1160  
 Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val Tyr Val Leu  
 360 365 370

cca cca tcc cca aag gag ttg tca tcc agt gac acg gtc acc ctg acc 1208  
 Pro Pro Ser Pro Lys Glu Leu Ser Ser Ser Asp Thr Val Thr Leu Thr  
 375 380 385

tgc ctg atc aaa gac ttc ttc cca cct gag att gat gtg gag tgg cag 1256  
 Cys Leu Ile Lys Asp Phe Phe Pro Pro Glu Ile Asp Val Glu Trp Gln  
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agc aat gga cag ccg gag ccc gag agc aag tac cac acg act gcg ccc 1304  
 Ser Asn Gly Gln Pro Glu Pro Glu Ser Lys Tyr His Thr Thr Ala Pro  
 405 410 415

cag ctg gac gag gac ggg tcc tac ttc ctg tac agc aag ctc tct gtg 1352  
 Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val  
 420 425 430 435

gac aag agc cgc tgg cag cag gga gac acc ttc aca tgt gcg gtg atg 1400  
 Asp Lys Ser Arg Trp Gln Gln Gly Asp Thr Phe Thr Cys Ala Val Met  
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cat gaa gct cta cag aac cac tac aca gat cta tcc ctc tcc cat tct 1448  
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 Pro Gly Gly Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe  
 35 40 45

Ser Asp Tyr Gly Met Ser Trp Val Arg Gln Ser Pro Gly Lys Gly Leu  
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Gln Trp Val Ala Ala Val Ser Asn Arg Gly Asp Thr Tyr Tyr Ala Asp  
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Ala Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr  
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Leu Tyr Leu Gln Met Ser Ser Leu Lys Ala Glu Asp Thr Ala Ile Tyr  
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His Cys Val Thr Gly Val Trp Pro Arg His Tyr Tyr Gly Met Asp His  
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Pro Ser Val Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser  
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Thr Val Ala Leu Ala Cys Leu Val Ser Gly Tyr Phe Pro Glu Pro Val  
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Thr Val Ser Trp Asn Ser Gly Ser Leu Thr Ser Gly Val His Thr Phe  
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Pro Ser Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Thr Val  
 195 200 205

Thr Val Pro Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val  
 210 215 220

Val His Pro Ala Ser Asn Thr Lys Val Asp Lys Pro Val Pro Lys Glu  
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Ser Thr Cys Lys Cys Ile Ser Pro Cys Pro Val Pro Glu Ser Leu Gly  
 245 250 255

Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg  
 260 265 270

Ile Thr Arg Thr Pro Glu Ile Thr Cys Val Val Leu Asp Leu Gly Arg  
 275 280 285

Glu Asp Pro Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val  
 290 295 300

His Thr Ala Lys Thr Gln Pro Arg Glu Gln Gln Phe Asn Ser Thr Tyr  
 305 310 315 320  
 Arg Val Val Ser Val Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly  
 325 330 335  
 Lys Glu Phe Lys Cys Arg Val Asn His Ile Gly Leu Pro Ser Pro Ile  
 340 345 350  
 Glu Arg Thr Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val  
 355 360 365  
 Tyr Val Leu Pro Pro Ser Pro Lys Glu Leu Ser Ser Ser Asp Thr Val  
 370 375 380  
 Thr Leu Thr Cys Leu Ile Lys Asp Phe Phe Pro Pro Glu Ile Asp Val  
 385 390 395 400  
 Glu Trp Gln Ser Asn Gly Gln Pro Glu Pro Glu Ser Lys Tyr His Thr  
 405 410 415  
 Thr Ala Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys  
 420 425 430  
 Leu Ser Val Asp Lys Ser Arg Trp Gln Gln Gly Asp Thr Phe Thr Cys  
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ctggtgctca atggggagga cgctgaccac acggtaggtg ctggtgaact gctgctcacg 480
aggctgcgtc ttggctgtgt gcacctcctt accatccacg aaccagctga tctgcacctc 540
agggtcctca cggcccagat ctaacaccac acaggtgatc tcgggtgttc gggtaatcct 600
gaggatgtcc ttgggtttcg ggggaaagat gaagaccgaa ggccctcca gtgattcagg 660
gactgggcat ggggatatac acttgacagg ggactctttg ggcactggct tgtctacttt 720
agtgttgctg gccgggtgga ccacgttgca ggtgaaggtc tcgctgggcc acctgctgga 780
gggcactgtc accgtgctgc tgagggagta gagccctgag gactgcagga cggacgggaa 840
ggtgtgcaca ccgctggtca aggagccgga attccaggac acagttacag gctcggggaa 900
gtagcctgac accaggcagg ccagggccac cgtggagccg gaagtggacc cgcagctggg 960
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gattgccgtg tcctcggctt tcaggctgct catctggaga tacagcgtgt tcttggcggt 1140
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gctaacagct gcgaccact gcagccctt ccttgagac tgacggacc aactcatgcc 1260
atagtcactg aaggtgaatc cagaggccac acaggacagt ctcaaggacc cccaggtt 1320
caccaggtct ccccagact ccaccagttg cacctcacc tggaacactt ttaaaataga 1380
gacaaggaaa acccagcaga gcacagactc catggtggtt tgtctgtgtt gtgtcctgag 1440
cactgaatgg ggtcacctgg                                     1460

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<210> 13

<211> 60

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (1)..(60)

<400> 13

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gcc aaa gaa tgc gag tgc aag tgt aac tgt aac aac tgc cca tgc cca 48
Ala Lys Glu Cys Glu Cys Lys Cys Asn Cys Asn Asn Cys Pro Cys Pro
  1             5             10             15

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ggt tgt ggc ctg 60
Gly Cys Gly Leu
      20

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<210> 14

<211> 20

<212> PRT

<213> Canis familiaris

<400> 14

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Ala Lys Glu Cys Glu Cys Lys Cys Asn Cys Asn Asn Cys Pro Cys Pro
  1             5             10             15

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Gly Cys Gly Leu  
20

<210> 15  
<211> 60  
<212> DNA  
<213> Canis familiaris

<400> 15  
caggccacaa cctgggcatg ggcagttggt acagttacac ttgcactcgc attctttggc 60

<210> 16  
<211> 1456  
<212> DNA  
<213> Canis familiaris

<220>  
<221> CDS  
<222> (32)..(1453)

<220>  
<221> misc\_feature  
<222> (27)  
<223> At position 27, n = unknown

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Met Glu Ser Val Leu Tyr Trp  
1 5  
  
gtt ttc ctt gtc gct att tta aag ggt gtc cag ggt gac gtg cag ctg 100  
Val Phe Leu Val Ala Ile Leu Lys Gly Val Gln Gly Asp Val Gln Leu  
10 15 20  
  
gtg gag tct ggg gga gac ctg gtg aag cct ggg ggg tcc ttg aga ctg 148  
Val Glu Ser Gly Gly Asp Leu Val Lys Pro Gly Gly Ser Leu Arg Leu  
25 30 35  
  
tcc tgt gtg gcc tct gga ttc acc ttt agt agc tgt gcc atg agc tgg 196  
Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Ser Cys Ala Met Ser Trp  
40 45 50 55  
  
gtc cgt cag tct cca ggg aag ggg cct cag tgg gtc gca act att cgg 244  
Val Arg Gln Ser Pro Gly Lys Gly Pro Gln Trp Val Ala Thr Ile Arg

60	65	70	
tat gat gga agt gat ata tac tac gca gac gct gtg aag ggc cga ttc			292
Tyr Asp Gly Ser Asp Ile Tyr Tyr Ala Asp Ala Val Lys Gly Arg Phe			
75	80	85	
agc atc tcc aga gac aac gcc aag aac acg gtg tat ctg cag atg aac			340
Ser Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu Gln Met Asn			
90	95	100	
agc ctg aga gcc gag gac acg gcc gtg tat tat tgt gcg aag gcc ccc			388
Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Ala Pro			
105	110	115	
ccc tac gat agt tac cac tat ggt atg gac tat tgg ggt cct ggc act			436
Pro Tyr Asp Ser Tyr His Tyr Gly Met Asp Tyr Trp Gly Pro Gly Thr			
120	125	130	135
tcc ctc ttc gtg tcg tca gcc tcc acc acg gcc ccc tcg gtt ttc cca			484
Ser Leu Phe Val Ser Ser Ala Ser Thr Thr Ala Pro Ser Val Phe Pro			
140	145	150	
ctg gcc ccc agc tgt ggg tcc caa tcc ggc tcc acg gtg gcc ctg gcc			532
Leu Ala Pro Ser Cys Gly Ser Gln Ser Gly Ser Thr Val Ala Leu Ala			
155	160	165	
tgc ctg gtg tca ggc tac atc ccc gag cct gta act gtg tcc tgg aat			580
Cys Leu Val Ser Gly Tyr Ile Pro Glu Pro Val Thr Val Ser Trp Asn			
170	175	180	
tcc gtc tcc ttg acc agc ggt gtg cac acc ttc ccg tcc gtc ctg cag			628
Ser Val Ser Leu Thr Ser Gly Val His Thr Phe Pro Ser Val Leu Gln			
185	190	195	
tcc tca ggg ctc tac tcc ctc agc agc atg gtg aca gtg ccc tcc agc			676
Ser Ser Gly Leu Tyr Ser Leu Ser Ser Met Val Thr Val Pro Ser Ser			
200	205	210	215
agg tgg ccc agc gag acc ttc acc tgc aat gtg gcc cac ccg gcc acc			724
Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val Ala His Pro Ala Thr			
220	225	230	
aac act aaa gta gac aag cca gtg gcc aaa gaa tgc gag tgc aag tgt			772
Asn Thr Lys Val Asp Lys Pro Val Ala Lys Glu Cys Glu Cys Lys Cys			
235	240	245	
aac tgt aac aac tgc cca tgc cca ggt tgt ggc ctg ctg gga ggg cct			820
Asn Cys Asn Asn Cys Pro Cys Pro Gly Cys Gly Leu Leu Gly Gly Pro			



250	255	260	
tcg gtc ttc atc ttt ccc cca aaa ccc aag gac atc ctc gtg act gcc			868
Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Val Thr Ala			
265	270	275	
cgg aca ccc aca gtc act tgt gtg gtg gtg gat ctg gac cca gaa aac			916
Arg Thr Pro Thr Val Thr Cys Val Val Val Asp Leu Asp Pro Glu Asn			
280	285	290	295
cct gag gtg cag atc agc tgg ttc gtg gat agt aag cag gtg caa aca			964
Pro Glu Val Gln Ile Ser Trp Phe Val Asp Ser Lys Gln Val Gln Thr			
300	305	310	
gcc aac acg cag cct cgt gag gag cag tcc aat ggc acc tac cgt gtg			1012
Ala Asn Thr Gln Pro Arg Glu Glu Gln Ser Asn Gly Thr Tyr Arg Val			
315	320	325	
gtc agt gtc ctc ccc att ggg cac cag gac tgg ctt tca ggg aag cag			1060
Val Ser Val Leu Pro Ile Gly His Gln Asp Trp Leu Ser Gly Lys Gln			
330	335	340	
ttc aag tgc aaa gtc aac aac aaa gcc ctc cca tcc ccc att gag gag			1108
Phe Lys Cys Lys Val Asn Asn Lys Ala Leu Pro Ser Pro Ile Glu Glu			
345	350	355	
atc atc tcc aag acc cca ggg cag gcc cat cag cct aat gtg tat gtc			1156
Ile Ile Ser Lys Thr Pro Gly Gln Ala His Gln Pro Asn Val Tyr Val			
360	365	370	375
ctg ccg cca tcg cgg gat gag atg agc aag aat acg gtc acc ctg acc			1204
Leu Pro Pro Ser Arg Asp Glu Met Ser Lys Asn Thr Val Thr Leu Thr			
380	385	390	
tgt ctg gtc aaa gac ttc ttc cca cct gag att gat gtg gag tgg cag			1252
Cys Leu Val Lys Asp Phe Phe Pro Pro Glu Ile Asp Val Glu Trp Gln			
395	400	405	
agc aat gga cag cag gag cct gag agc aag tac cgc atg acc ccg ccc			1300
Ser Asn Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg Met Thr Pro Pro			
410	415	420	
cag ctg gat gaa gat ggg tcc tac ttc cta tac agc aag ctc tcc gtg			1348
Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val			
425	430	435	
gac aag agc cgc tgg cag cgg gga gac acc ttc ata tgt gcg gtg atg			1396
Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile Cys Ala Val Met			

440                      445                      450                      455  
 cat gaa gct cta cac aac cac tac aca cag ata tcc ctc tcc cat tct    1444  
 His Glu Ala Leu His Asn His Tyr Thr Gln Ile Ser Leu Ser His Ser  
                     460                      465                      470  
  
 ccg ggt aaa tga    1456  
 Pro Gly Lys  
  
 <210> 17  
 <211> 474  
 <212> PRT  
 <213> Canis familiaris  
  
 <400> 17  
 Met Glu Ser Val Leu Tyr Trp Val Phe Leu Val Ala Ile Leu Lys Gly  
     1                      5                      10                      15  
  
 Val Gln Gly Asp Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys  
                     20                      25                      30  
  
 Pro Gly Gly Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe  
                     35                      40                      45  
  
 Ser Ser Cys Ala Met Ser Trp Val Arg Gln Ser Pro Gly Lys Gly Pro  
                     50                      55                      60  
  
 Gln Trp Val Ala Thr Ile Arg Tyr Asp Gly Ser Asp Ile Tyr Tyr Ala  
     65                      70                      75                      80  
  
 Asp Ala Val Lys Gly Arg Phe Ser Ile Ser Arg Asp Asn Ala Lys Asn  
                     85                      90                      95  
  
 Thr Val Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val  
                     100                      105                      110  
  
 Tyr Tyr Cys Ala Lys Ala Pro Pro Tyr Asp Ser Tyr His Tyr Gly Met  
                     115                      120                      125  
  
 Asp Tyr Trp Gly Pro Gly Thr Ser Leu Phe Val Ser Ser Ala Ser Thr  
                     130                      135                      140  
  
 Thr Ala Pro Ser Val Phe Pro Leu Ala Pro Ser Cys Gly Ser Gln Ser  
     145                      150                      155                      160  
  
 Gly Ser Thr Val Ala Leu Ala Cys Leu Val Ser Gly Tyr Ile Pro Glu  
                     165                      170                      175

Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Val	Ser	Leu	Thr	Ser	Gly	Val	His	180	185	190
Thr	Phe	Pro	Ser	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	195	200	205
Met	Val	Thr	Val	Pro	Ser	Ser	Arg	Trp	Pro	Ser	Glu	Thr	Phe	Thr	Cys	210	215	220
Asn	Val	Ala	His	Pro	Ala	Thr	Asn	Thr	Lys	Val	Asp	Lys	Pro	Val	Ala	225	230	235
Lys	Glu	Cys	Glu	Cys	Lys	Cys	Asn	Cys	Asn	Asn	Cys	Pro	Cys	Pro	Gly	245	250	255
Cys	Gly	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Pro	260	265	270
Lys	Asp	Ile	Leu	Val	Thr	Ala	Arg	Thr	Pro	Thr	Val	Thr	Cys	Val	Val	275	280	285
Val	Asp	Leu	Asp	Pro	Glu	Asn	Pro	Glu	Val	Gln	Ile	Ser	Trp	Phe	Val	290	295	300
Asp	Ser	Lys	Gln	Val	Gln	Thr	Ala	Asn	Thr	Gln	Pro	Arg	Glu	Glu	Gln	305	310	315
Ser	Asn	Gly	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Pro	Ile	Gly	His	Gln	325	330	335
Asp	Trp	Leu	Ser	Gly	Lys	Gln	Phe	Lys	Cys	Lys	Val	Asn	Asn	Lys	Ala	340	345	350
Leu	Pro	Ser	Pro	Ile	Glu	Glu	Ile	Ile	Ser	Lys	Thr	Pro	Gly	Gln	Ala	355	360	365
His	Gln	Pro	Asn	Val	Tyr	Val	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Met	Ser	370	375	380
Lys	Asn	Thr	Val	Thr	Leu	Thr	Cys	Leu	Val	Lys	Asp	Phe	Phe	Pro	Pro	385	390	395
Glu	Ile	Asp	Val	Glu	Trp	Gln	Ser	Asn	Gly	Gln	Gln	Glu	Pro	Glu	Ser	405	410	415
Lys	Tyr	Arg	Met	Thr	Pro	Pro	Gln	Leu	Asp	Glu	Asp	Gly	Ser	Tyr	Phe	420	425	430

Leu Tyr Ser Lys Leu Ser Val Asp Lys Ser Arg Trp Gln Arg Gly Asp  
 435 440 445

Thr Phe Ile Cys Ala Val Met His Glu Ala Leu His Asn His Tyr Thr  
 450 455 460

Gln Ile Ser Leu Ser His Ser Pro Gly Lys  
 465 470

<210> 18

<211> 1456

<212> DNA

<213> Canis familiaris

<220>

<221> misc\_feature

<222> (1430)

<223> At position 1430, n = unknown

<400> 18

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catcaccgca catatgaagg tgtctccccg ctgccagcgg ctcttgtcca cggagagctt 120
gctgtatagg aagtaggacc catcttcatc cagctggggc ggggtcatgc ggtacttgct 180
ctcaggctcc tgctgtccat tgctctgcca ctccacatca atctcagggtg ggaagaagtc 240
tttgaccaga caggtcaggg tgaccgtatt cttgctcatc tcatccccg atggcgccag 300
gacatacaca ttaggctgat gggcctgccc tggggtcttg gagatgatct cctcaatggg 360
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gtgcccgaatg gggaggacac tgaccacacg gtaggtgcca ttggactgct cctcacgagg 480
ctgcgtgttg gctgtttgca cctgcttact atccacgaac cagctgatct gcacctcagg 540
gttttctggg tccagatcca ccaccacaca agtgactgtg ggtgtccggg cagtcacgag 600
gatgtccttg ggttttgggg gaaagatgaa gaccgaaggc cctcccagca ggccacaacc 660
tgggcatggg cagttgttac agttacactt gcaactcgcat tctttggcca ctggcttgtc 720
tacttttagtg ttggtggccg ggtggggccac attgcagggtg aagggtctgc tggggccacct 780
gctggagggc actgtcacca tgctgctgag ggagtagagc cctgaggact gcaggacgga 840
cggaagggtg tgcacaccgc tggtaagga gacggaattc caggacacag ttacaggctc 900
ggggatgtag cctgacacca ggcaggccag ggccaccgtg gagccggatt gggaccaca 960
gctggggggc agtgggaaaa ccgagggggc cgtggtggag gctgacgaca cgaagaggga 1020
agtgccagga cccaatagt ccataccata gtggaacta tcgtaggggg gggccttcgc 1080
acaataatac acggccgtgt cctcggtctc caggctgttc atctgcagat acaccgtgtt 1140
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1456

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<210> 19
<211> 1453
<212> DNA
<213> Canis familiaris
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1 5																	
gtt ttc ctt gtc act att tta aaa ggt gtc cag ggt gag gta cgt ttg																	100
Val Phe Leu Val Thr Ile Leu Lys Gly Val Gln Gly Glu Val Arg Leu																	
10 15 20																	
gtg gag tct gga gga acc ctg gtg aag cct ggg ggg tcc ctg aaa ctc																	148
Val Glu Ser Gly Gly Thr Leu Val Lys Pro Gly Gly Ser Leu Lys Leu																	
25 30 35																	
tct tgt gtg gcc tct gga ttc acc ttc aga aga tac tcc atg gac tgg																	196
Ser Cys Val Ala Ser Gly Phe Thr Phe Arg Arg Tyr Ser Met Asp Trp																	
40 45 50 55																	
gtc cgc cag gct cca ggc aag agc ctg cag tgg gtc gcc ggg att aac																	244
Val Arg Gln Ala Pro Gly Lys Ser Leu Gln Trp Val Ala Gly Ile Asn																	
60 65 70																	
ggg gat ggc aca gga aca tcc tat tca cag act gtg aag ggc cga ttc																	292
Gly Asp Gly Thr Gly Thr Ser Tyr Ser Gln Thr Val Lys Gly Arg Phe																	
75 80 85																	
acc atc tcc aga gac aac gcc aag aac acc ctc tat ctg cag ata aac																	340
Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu Gln Ile Asn																	
90 95 100																	
agc ctg aga gcc gaa gac tct gct gtg tat tat tgt gcc aag agc tgg																	388
Ser Leu Arg Ala Glu Asp Ser Ala Val Tyr Tyr Cys Ala Lys Ser Trp																	
105 110 115																	
tct cgt aat ggg gat ctt gac tac tgg ggc cag gga acc ctg gtc acc																	436
Ser Arg Asn Gly Asp Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr																	
120 125 130 135																	

gtc tcc tca gcc tcc acc acg gcc ccc tcg gtt ttc cca ctg gcc ccc	484
Val Ser Ser Ala Ser Thr Thr Ala Pro Ser Val Phe Pro Leu Ala Pro	
140 145 150	
agc tgc ggg tcc act tcc ggc tcc acg gtg gcc ctg gcc tgc ctg gtg	532
Ser Cys Gly Ser Thr Ser Gly Ser Thr Val Ala Leu Ala Cys Leu Val	
155 160 165	
tca ggc tac ttc ccc gag cct gta act gtg tcc tgg aat tcc ggc tcc	580
Ser Gly Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ser	
170 175 180	
ttg acc agc ggt gtg cac acc ttc ccg tcc gtc ctg cag tcc tca ggg	628
Leu Thr Ser Gly Val His Thr Phe Pro Ser Val Leu Gln Ser Ser Gly	
185 190 195	
ctc tac tcc ctc agc agc atg gtg aca gtg ccc tcc agc agg tgg ccc	676
Leu Tyr Ser Leu Ser Ser Met Val Thr Val Pro Ser Ser Arg Trp Pro	
200 205 210 215	
agc gag acc ttc acc tgc aac gtg gcc cac ccg gcc agc aaa act aaa	724
Ser Glu Thr Phe Thr Cys Asn Val Ala His Pro Ala Ser Lys Thr Lys	
220 225 230	
gta gac aag cca gtg ccc aaa aga gaa aat gga aga gtt cct cgc cca	772
Val Asp Lys Pro Val Pro Lys Arg Glu Asn Gly Arg Val Pro Arg Pro	
235 240 245	
cct gat tgt ccc aaa tgc cca gcc cct gaa atg ctg gga ggg cct tcg	820
Pro Asp Cys Pro Lys Cys Pro Ala Pro Glu Met Leu Gly Gly Pro Ser	
250 255 260	
gtc ttc atc ttt ccc ccg aaa ccc aag gac acc ctc ttg att gcc cga	868
Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Thr Leu Leu Ile Ala Arg	
265 270 275	
aca cct gag gtc aca tgt gtg gtg gtg gat ctg gac cca gaa gac cct	916
Thr Pro Glu Val Thr Cys Val Val Val Asp Leu Asp Pro Glu Asp Pro	
280 285 290 295	
gag gtg cag atc agc tgg ttc gtg gac ggt aag cag atg caa aca gcc	964
Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Gln Met Gln Thr Ala	
300 305 310	
aag act cag cct cgt gag gag cag ttc aat ggc acc tac cgt gtg gtc	1012
Lys Thr Gln Pro Arg Glu Glu Gln Phe Asn Gly Thr Tyr Arg Val Val	
315 320 325	

agt gtc ctc ccc att ggg cac cag gac tgg ctc aag ggg aag cag ttc	1060
Ser Val Leu Pro Ile Gly His Gln Asp Trp Leu Lys Gly Lys Gln Phe	
330 335 340	
acg tgc aaa gtc aac aac aaa gcc ctc cca tcc ccg atc gag agg acc	1108
Thr Cys Lys Val Asn Asn Lys Ala Leu Pro Ser Pro Ile Glu Arg Thr	
345 350 355	
atc tcc aag gcc aga ggg caa gcc cat cag ccc agt gtg tat gtc ctg	1156
Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val Tyr Val Leu	
360 365 370 375	
ccg cca tcc cgg gag gag ttg agc aag aac aca gtc agc ttg aca tgc	1204
Pro Pro Ser Arg Glu Glu Leu Ser Lys Asn Thr Val Ser Leu Thr Cys	
380 385 390	
ctg atc aaa gac ttc ttc cca cct gac att gat gtg gag tgg cag agc	1252
Leu Ile Lys Asp Phe Phe Pro Pro Asp Ile Asp Val Glu Trp Gln Ser	
395 400 405	
aat gga cag cag gag cct gag agc aag tac cgc acg acc ccg ccc cag	1300
Asn Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg Thr Thr Pro Pro Gln	
410 415 420	
ctg gac gag gac ggg tcc tac ttc ctg tac agc aag ctc tct gtg gac	1348
Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp	
425 430 435	
aag agc cgc tgg cag cgg gga gac acc ttc ata tgt gcg gtg atg cat	1396
Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile Cys Ala Val Met His	
440 445 450 455	
gaa gct cta cac aac cac tac aca cag gaa tcc ctc tcc cat tct ccg	1444
Glu Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser His Ser Pro	
460 465 470	
ggt aaa tga	1453
Gly Lys	

<210> 20  
 <211> 473  
 <212> PRT  
 <213> Canis familiaris

<400> 20  
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 1 5 10 15

Val	Gln	Gly	Glu	Val	Arg	Leu	Val	Glu	Ser	Gly	Gly	Thr	Leu	Val	Lys			
			20					25					30					
Pro	Gly	Gly	Ser	Leu	Lys	Leu	Ser	Cys	Val	Ala	Ser	Gly	Phe	Thr	Phe			
		35					40					45						
Arg	Arg	Tyr	Ser	Met	Asp	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Ser	Leu			
		50				55					60							
Gln	Trp	Val	Ala	Gly	Ile	Asn	Gly	Asp	Gly	Thr	Gly	Thr	Ser	Tyr	Ser			
	65				70					75					80			
Gln	Thr	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn			
				85					90					95				
Thr	Leu	Tyr	Leu	Gln	Ile	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Ser	Ala	Val			
			100					105					110					
Tyr	Tyr	Cys	Ala	Lys	Ser	Trp	Ser	Arg	Asn	Gly	Asp	Leu	Asp	Tyr	Trp			
		115					120					125						
Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Thr	Ala	Pro			
	130					135					140							
Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Cys	Gly	Ser	Thr	Ser	Gly	Ser	Thr			
145					150					155					160			
Val	Ala	Leu	Ala	Cys	Leu	Val	Ser	Gly	Tyr	Phe	Pro	Glu	Pro	Val	Thr			
				165					170					175				
Val	Ser	Trp	Asn	Ser	Gly	Ser	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro			
			180					185					190					
Ser	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Met	Val	Thr			
		195					200					205						
Val	Pro	Ser	Ser	Arg	Trp	Pro	Ser	Glu	Thr	Phe	Thr	Cys	Asn	Val	Ala			
	210					215					220							
His	Pro	Ala	Ser	Lys	Thr	Lys	Val	Asp	Lys	Pro	Val	Pro	Lys	Arg	Glu			
225					230					235					240			
Asn	Gly	Arg	Val	Pro	Arg	Pro	Pro	Asp	Cys	Pro	Lys	Cys	Pro	Ala	Pro			
			245						250					255				
Glu	Met	Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Pro	Lys			
			260					265					270					



Asp Thr Leu Leu Ile Ala Arg Thr Pro Glu Val Thr Cys Val Val Val		
275	280	285
Asp Leu Asp Pro Glu Asp Pro Glu Val Gln Ile Ser Trp Phe Val Asp		
290	295	300
Gly Lys Gln Met Gln Thr Ala Lys Thr Gln Pro Arg Glu Glu Gln Phe		
305	310	315 320
Asn Gly Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gly His Gln Asp		
	325	330 335
Trp Leu Lys Gly Lys Gln Phe Thr Cys Lys Val Asn Asn Lys Ala Leu		
	340	345 350
Pro Ser Pro Ile Glu Arg Thr Ile Ser Lys Ala Arg Gly Gln Ala His		
	355	360 365
Gln Pro Ser Val Tyr Val Leu Pro Pro Ser Arg Glu Glu Leu Ser Lys		
	370	375 380
Asn Thr Val Ser Leu Thr Cys Leu Ile Lys Asp Phe Phe Pro Pro Asp		
385	390	395 400
Ile Asp Val Glu Trp Gln Ser Asn Gly Gln Gln Glu Pro Glu Ser Lys		
	405	410 415
Tyr Arg Thr Thr Pro Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu		
	420	425 430
Tyr Ser Lys Leu Ser Val Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr		
	435	440 445
Phe Ile Cys Ala Val Met His Glu Ala Leu His Asn His Tyr Thr Gln		
	450	455 460
Glu Ser Leu Ser His Ser Pro Gly Lys		
465	470	

<210> 21  
 <211> 1453  
 <212> DNA  
 <213> Canis familiaris  
  
 <400> 21

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tcattttaccc ggagaatggg agaggggattc ctgtgtgtag tgggttggtga gagcttcatg 60
catcaccgca catatgaagg tgtctccccg ctgccagcgg ctcttgtcca cagagagctt 120
gctgtacagg aagtaggacc cgtcctcgtc cagctggggc ggggtcgtgc ggtacttgct 180
ctcaggctcc tgcgtgccat tgcctcgcca ctccacatca atgtcaggtg ggaagaagtc 240
tttgatcagg catgtcaagc tgactgtgtt ctgtctcaac tctccccggg atggcggcag 300
gacatacaca ctgggctgat gggcttgccc tctggccttg gagatgggtc tctcgatcgg 360
ggatgggagg gctttgttgt tgactttgca cgtgaactgc tcccccttga gccagtcctg 420
gtgcccgaatg gggaggacac tgaccacacg gtaggtgcca ttgaactgct cctcacgagg 480
ctgagtccttg gctgtttgca tctgcttacc gtccacgaac cagctgatct gcacctcagg 540
gtcttctggg tccagatcca ccaccacaca tgtgacctca ggtgttcggg caatcaagag 600
ggtgtccttg ggtttcgggg gaaagatgaa gaccgaaggc cctcccagca tttcaggggc 660
tgggcatttg ggacaatcag gtgggcgagg aactcttcca ttttctcttt tgggcactgg 720
cttgtctact ttagttttgc tggccgggtg ggccacgttg caggtgaagg tctcgctggg 780
ccacctgctg gagggcactg tcaccatgct gctgaggagg tagagccctg aggactgcag 840
gacggacggg aaggtgtgca caccgctggt caaggagccg gaattccagg acacagttac 900
aggctcgggg aagtagcctg acaccaggca ggccagggcc accgtggagc cggaagtgga 960
cccgcagctg ggggccagtg ggaaaaccga gggggccgtg gtggaggctg aggagacggt 1020
gaccaggggt ccctggcccc agtagtcaag atccccatta cgagaccagc tcttggcaca 1080
ataatacaca gcagagtctt cggctctcag gctgtttatc tgcagataga ggggtgttctt 1140
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gccatcaccg ttaatcccg cgacccactg caggtctctg cctggagcct ggcggaccca 1260
gtccatggag tatcttctga aggtgaatcc agaggccaca caagagagtt tcagggaccc 1320
cccaggcttc accagggttc ctccagactc caccaaactg acctcaccct ggacaccttt 1380
taaaatagtg acaaggaaaa ccagaagag cacagactcc atggtgattt gtctgtgtgg 1440
tgtcctgagc act 1453

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<210> 22

<211> 66

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (1)..(66)

<400> 22

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ccc aaa aga gaa aat gga aga gtt cct cgc cca cct gat tgt ccc aaa 48
Pro Lys Arg Glu Asn Gly Arg Val Pro Arg Pro Pro Asp Cys Pro Lys
1 5 10 15

```

```

tgc cca gcc cct gaa atg 66
Cys Pro Ala Pro Glu Met
20

```

<210> 23

<211> 22

<212> PRT

<213> Canis familiaris

<400> 23

Pro Lys Arg Glu Asn Gly Arg Val Pro Arg Pro Pro Asp Cys Pro Lys  
1 5 10 15

Cys Pro Ala Pro Glu Met  
20

<210> 24

<211> 66

<212> DNA

<213> Canis familiaris

<400> 24

catttcaggg gctgggcatt tgggacaatc aggtgggcga ggaactcttc cattttctct 60  
tttggg 66

<210> 25

<211> 938

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (37)..(753)

<220>

<221> misc\_feature

<222> (475)

<223> At position 475, n = unknown, and at amino acid  
position 147, Xaa = unknown

<400> 25

ggcacgaggg tccccagaag gcaggatcaa tcagtg atg tcc tcc gac atg gcc 54  
Met Ser Ser Asp Met Ala  
1 5

tgg tcc cct ctc ctc ctc aca ctc ctc gct cac tgc aca ggg tcc tgg 102  
Trp Ser Pro Leu Leu Leu Thr Leu Leu Ala His Cys Thr Gly Ser Trp  
10 15 20

gcc cag gct gtg ttg aat cag ccg gcc tca gta tct ggg gcc ctg ggc 150  
Ala Gln Ala Val Leu Asn Gln Pro Ala Ser Val Ser Gly Ala Leu Gly

25	30	35	
cag aag gtc acc atc tcc tgc tct gga gac acg aat gac att gat ata			198
Gln Lys Val Thr Ile Ser Cys Ser Gly Asp Thr Asn Asp Ile Asp Ile			
40	45	50	
ttc ggt gtg aac tgg tac caa caa ctc cca gga aag gcc cct aca gtc			246
Phe Gly Val Asn Trp Tyr Gln Gln Leu Pro Gly Lys Ala Pro Thr Val			
55	60	65	70
ctc gtg gac agt gat ggg gat cga ccc tca ggg gtc cct gac aga ttt			294
Leu Val Asp Ser Asp Gly Asp Arg Pro Ser Gly Val Pro Asp Arg Phe			
75	80	85	
tct ggc tcc agt tct ggc aac tca ggc acc ctg acc atc act ggg ctc			342
Ser Gly Ser Ser Ser Gly Asn Ser Gly Thr Leu Thr Ile Thr Gly Leu			
90	95	100	
cag gct gag gac gag gct gat tat tac tgt cag tct gtt gat tcc acg			390
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Val Asp Ser Thr			
105	110	115	
ctt ggt gtt tac gtg ttc ggc tca gga acc caa ctg act gtc ctt ggt			438
Leu Gly Val Tyr Val Phe Gly Ser Gly Thr Gln Leu Thr Val Leu Gly			
120	125	130	
cag ccc aag gcc tcc ccc tcg gtc aca ctc ttc ccg ncc tyc tyt gag			486
Gln Pro Lys Ala Ser Pro Ser Val Thr Leu Phe Pro Xaa Xaa Xaa Glu			
135	140	145	150
gag ctc ggc gcc aac aag gcc acc ctg gtg tgc ctc atc agc gac ttc			534
Glu Leu Gly Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe			
155	160	165	
tac ccc arc ggc gtg acg gtg gcc tgg aag gca gac ggc agc ccc gtc			582
Tyr Pro Xaa Gly Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val			
170	175	180	
acc cag ggc gtg gag acc acc aag ccc tcc aag cag agc aac aac aag			630
Thr Gln Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys			
185	190	195	
tac gcg gcc agc agc tac ctg agc ctg acg cct gac aag tgg aaa tct			678
Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Asp Lys Trp Lys Ser			
200	205	210	
cac agc agc ttc agc tgc ctg gtc acg cat gag ggg agc ccc gtg gaa			726
His Ser Ser Phe Ser Cys Leu Val Thr His Glu Gly Ser Pro Val Glu			

215                                      220                                      225                                      230  
 aaa aag gtg gcc ccc gca aag tgc tct taggttcccg atgccccccg                      773  
 Lys Lys Val Ala Pro Ala Lys Cys Ser  
    235  
 cccaccaaag ggggctcaaa gcctcaggac ctccaggagg atcttgccctc ccatctgggt 833  
 catcccagcc attcccctta aaccaggga acattcaata aagtgttctt tcttcaatca 893  
 gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa                                      938  
  
 <210> 26  
 <211> 239  
 <212> PRT  
 <213> Canis familiaris  
  
 <400> 26  
 Met Ser Ser Asp Met Ala Trp Ser Pro Leu Leu Leu Thr Leu Leu Ala  
     1                                      5                                      10                                      15  
 His Cys Thr Gly Ser Trp Ala Gln Ala Val Leu Asn Gln Pro Ala Ser  
    20                                      25                                      30  
 Val Ser Gly Ala Leu Gly Gln Lys Val Thr Ile Ser Cys Ser Gly Asp  
    35                                      40                                      45  
 Thr Asn Asp Ile Asp Ile Phe Gly Val Asn Trp Tyr Gln Gln Leu Pro  
    50                                      55                                      60  
 Gly Lys Ala Pro Thr Val Leu Val Asp Ser Asp Gly Asp Arg Pro Ser  
     65                                      70                                      75                                      80  
 Gly Val Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Ser Gly Thr  
    85                                      90                                      95  
 Leu Thr Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys  
    100                                      105                                      110  
 Gln Ser Val Asp Ser Thr Leu Gly Val Tyr Val Phe Gly Ser Gly Thr  
    115                                      120                                      125  
 Gln Leu Thr Val Leu Gly Gln Pro Lys Ala Ser Pro Ser Val Thr Leu  
    130                                      135                                      140  
 Phe Pro Xaa Xaa Xaa Glu Glu Leu Gly Ala Asn Lys Ala Thr Leu Val  
     145                                      150                                      155                                      160

Cys Leu Ile Ser Asp Phe Tyr Pro Xaa Gly Val Thr Val Ala Trp Lys  
                   165                  170                  175  
 Ala Asp Gly Ser Pro Val Thr Gln Gly Val Glu Thr Thr Lys Pro Ser  
                   180                  185                  190  
 Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr  
                   195                  200                  205  
 Pro Asp Lys Trp Lys Ser His Ser Ser Phe Ser Cys Leu Val Thr His  
                   210                  215                  220  
 Glu Gly Ser Pro Val Glu Lys Lys Val Ala Pro Ala Lys Cys Ser  
                   225                  230                  235

<210> 27  
 <211> 938  
 <212> DNA  
 <213> Canis familiaris  
  
 <220>  
 <221> misc\_feature  
 <222> (464)  
 <223> At osition 464, n = unknown

<400> 27  
 tttttttttt tttttttttt tttttttttt tttttttttt ttttctgatt gaagaaagaa 60  
 cactttattg aatgttgcc tgggtttaagg ggaatggctg ggatgacca gatgggaggc 120  
 aagatcctcc tggaggtcct gaggccttga gccccctttg gtgggcgggg ggcacgaggc 180  
 acctaagagc actttgctgg ggccaccttt ttttccacgg ggctcccctc atgcgtgacc 240  
 aggcagctga agctgctgtg agatttccac ttgtcaggcg tcaggctcag gtagctgctg 300  
 gccgcgtact tgttggtgct ctgcttggag ggcttgggtg tctccacgcc ctgggtgacg 360  
 gggctgccgt ctgccttcca ggccaccgtc acgccgytgg ggtagaagtc gctgatgagg 420  
 cacaccaggg tggccttggt ggccgccgag tcctcaragr agnccgggaa gagggtgacc 480  
 gagggggagg ccttgggctg accaaggaca gtcagttggg ttcttgagcc gaacacgtaa 540  
 acaccaagcg tggatcaaac agactgacag taataatcag cctcgtcctc agcctggagc 600  
 ccagtgatgg tcagggtgcc tgagttgcca gaactggagc cagaaaatct gtcagggacc 660  
 cctgagggtc gatccccatc actgtccacg aggactgtag gggcctttcc tgggagttgt 720  
 tgggtaccagt tcacaccgaa tatatcaatg tcattcgtgt ctccagagca ggagatggtg 780  
 accttctggc ccagggtccc agatactgag gccggctgat tcaacacagc ctggggccag 840  
 gaccctgtgc agtgagcgag gagggtgagg aggagagggg accaggccat gtcggaggac 900  
 atcactgatt gatcctgcct tctggggacc ctctgtgc 938

<210> 28

<211> 578  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> CDS  
 <222> (1)..(423)

<220>  
 <221> misc\_feature  
 <222> (471)  
 <223> At position 481, n = unknown

<220>  
 <221> misc\_feature  
 <222> (481)  
 <223> At position 481, n = unknown

<220>  
 <221> misc\_feature  
 <222> (522)  
 <223> At position 522, n = unknown

<220>  
 <221> misc\_feature  
 <222> (549)  
 <223> At position 549, n = unknown

<400> 28  
 cat caa gat tgg ttt aat ggt aag gag ttc aaa tgt aga gtc aac cac 48  
 His Gln Asp Trp Phe Asn Gly Lys Glu Phe Lys Cys Arg Val Asn His  
     1                    5                    10                    15

ata gac ctc ccg tct ccc atc gag agg acc atc tct aag gcc aga ggg 96  
 Ile Asp Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser Lys Ala Arg Gly  
                     20                    25                    30

agg gcc cat aag ccc agt gtg tat gtc ctg ccg cca tcc cca aag gag 144  
 Arg Ala His Lys Pro Ser Val Tyr Val Leu Pro Pro Ser Pro Lys Glu  
                     35                    40                    45

ttg tca tcc agt gac aca gtc agc atc acc tgc ctg ata aaa gac ttc 192  
 Leu Ser Ser Ser Asp Thr Val Ser Ile Thr Cys Leu Ile Lys Asp Phe  
                     50                    55                    60

tac cca cct gac att gat gtg gag tgg cag agc aat gga cag cag gag 240  
 Tyr Pro Pro Asp Ile Asp Val Glu Trp Gln Ser Asn Gly Gln Gln Glu  
                     65                    70                    75                    80

cct gag agc aag tac cgc acg acc ccg ccc cag ctg gac gag gac ggg 288  
 Pro Glu Ser Lys Tyr Arg Thr Thr Pro Pro Gln Leu Asp Glu Asp Gly  
                     85                    90                    95

tcc tac ttc ctg tac agc aag ctc tct gtg gac aag agc cgc tgg cag 336  
 Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys Ser Arg Trp Gln  
                     100                    105                    110

cgg gga gac acc ttc ata tgt gcg gtg atg cat gaa gct cta cac aac 384  
 Arg Gly Asp Thr Phe Ile Cys Ala Val Met His Glu Ala Leu His Asn  
                     115                    120                    125

cac tac aca cag aaa tcc ctc tcc cat tct ccg ggt aaa tgagcaacac 433  
 His Tyr Thr Gln Lys Ser Leu Ser His Ser Pro Gly Lys  
                     130                    135                    140

gcccggcacc cagcaagccc cccacccttg gctctcanga tccctganga cacctgagcc 493

cctgtccctg tgtacataac cctgggtang caccatcat gaaataaagc acccancact 553

gccctggggc cttgcaaaaa aaaaa 578

<210> 29

<211> 141

<212> PRT

<213> Canis familiaris

<400> 29

His Gln Asp Trp Phe Asn Gly Lys Glu Phe Lys Cys Arg Val Asn His  
     1                    5                    10                    15

Ile Asp Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser Lys Ala Arg Gly  
                     20                    25                    30

Arg Ala His Lys Pro Ser Val Tyr Val Leu Pro Pro Ser Pro Lys Glu  
                     35                    40                    45

Leu Ser Ser Ser Asp Thr Val Ser Ile Thr Cys Leu Ile Lys Asp Phe  
                     50                    55                    60

Tyr Pro Pro Asp Ile Asp Val Glu Trp Gln Ser Asn Gly Gln Gln Glu  
                     65                    70                    75                    80

Pro Glu Ser Lys Tyr Arg Thr Thr Pro Pro Gln Leu Asp Glu Asp Gly  
                     85                    90                    95



Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys Ser Arg Trp Gln  
100 105 110

Arg Gly Asp Thr Phe Ile Cys Ala Val Met His Glu Ala Leu His Asn  
115 120 125

His Tyr Thr Gln Lys Ser Leu Ser His Ser Pro Gly Lys  
130 135 140

<210> 30  
<211> 578  
<212> DNA  
<213> Canis familiaris

<220>  
<221> misc\_feature  
<222> (30)  
<223> At position 30, n = unknown

<220>  
<221> misc\_feature  
<222> (57)  
<223> At position 57, n = unknown

<220>  
<221> misc\_feature  
<222> (98)  
<223> At position 98, n = unknown

<220>  
<221> misc\_feature  
<222> (108)  
<223> At position 108, n = unknown

<400> 30  
tttttttttt gcaagggccc agggcagtg tgggtgcttt atttcatgat ggggtgcntac 60  
ccagggttat gtacacaggg acaggggctc aggtgtcntc agggatcntg agagccaagg 120  
gtgggggggct tgctgggtgc cgggcgtggt gctcatttac ccggagaatg ggagagggat 180  
ttctgtgtgt agtgggtgtg tagagcttca tgcattaccg cacatatgaa ggtgtctccc 240  
cgctgccagc ggctcttgct cacagagagc ttgctgtaca ggaagtagga cccgtcctcg 300  
tccagctggg gcggggctgt gcggtacttg ctctcaggct cctgctgtcc attgctctgc 360  
cactccacat caatgtcagg tgggtagaag tcttttatca ggcaggatgat gctgactgtg 420  
tacttgatg acaactcctt tggggatggc ggcaggacat acacactggg cttatgggcc 480  
ctccctctgg ccttagagat ggtcctctcg atgggagacg ggaggtctat gtggttgact 540  
ctacatttga actccttacc attaaaccaa tcttgatg 578

<210> 31  
 <211> 1364  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> CDS  
 <222> (59)..(1183)

<400> 31  
 ggcacgaggc cgattcacca tttccagaga caatgtcgag aacacgctgt atctgcag 58

atg aac agc ctg aga gct gag gat acg gcc ctg tat tac tgt aca agt 106  
 Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys Thr Ser  
 1 5 10 15

ggg tta tgg atc aac tgg tac ggt ccg aat ttt gac tcc tgg ggc cag 154  
 Gly Leu Trp Ile Asn Trp Tyr Gly Pro Asn Phe Asp Ser Trp Gly Gln  
 20 25 30

gga acc ctg gtc acc gtc tcc tca gcc tcc acc acg gcc ccc tcg gtt 202  
 Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Thr Ala Pro Ser Val  
 35 40 45

ttc cca ctg gcc ccc agc tgc ggg tcc act tcc ggc tcc acg gtg gcc 250  
 Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser Thr Val Ala  
 50 55 60

ctg gcc tgc ctg gtg tca ggc tac ttc ccc gag cct gta act gtg tcc 298  
 Leu Ala Cys Leu Val Ser Gly Tyr Phe Pro Glu Pro Val Thr Val Ser  
 65 70 75 80

tgg aat tcc ggc tcc ttg acc agc ggt gtg cac acc ttc ccg tcc gtc 346  
 Trp Asn Ser Gly Ser Leu Thr Ser Gly Val His Thr Phe Pro Ser Val  
 85 90 95

ctg cag tcc tca ggg ctc tac tcc ctc agc agc atg gtg aca gtg ccc 394  
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Met Val Thr Val Pro  
 100 105 110

tcc agc agg tgg ccc agc gag acc ttc acc tgc aac gtg gcc cac ccg 442  
 Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val Ala His Pro  
 115 120 125

gcc agc aaa act aaa gta gac aag cca gtg ccc aaa aga gaa aat gga 490  
 Ala Ser Lys Thr Lys Val Asp Lys Pro Val Pro Lys Arg Glu Asn Gly  
 130 135 140

aga gtt cct cgc cca cct gat tgt ccc aaa tgc cca acc cct gaa atg	538
Arg Val Pro Arg Pro Pro Asp Cys Pro Lys Cys Pro Thr Pro Glu Met	
145 150 155 160	
ctg gga ggg cct tcg gtc ttc atc ttt ccc ccg aaa ccc aag gac acc	586
Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Thr	
165 170 175	
ctc ttg att gcc cga aca cct gag gtc aca tgt gtg gtg gtg gat ctg	634
Leu Leu Ile Ala Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Leu	
180 185 190	
gac cca gaa gac cct gag gtg cag atc agc tgg ttc gtg gac ggt aag	682
Asp Pro Glu Asp Pro Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys	
195 200 205	
cag atg caa aca gcc aag act cag cct cgt gag gag cag ttc aat ggc	730
Gln Met Gln Thr Ala Lys Thr Gln Pro Arg Glu Glu Gln Phe Asn Gly	
210 215 220	
acc tac cgt gtg gtc agt gtc ctc ccc att ggg cac cag gac tgg ctc	778
Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gly His Gln Asp Trp Leu	
225 230 235 240	
aag ggg aag cag ttc acg tgc aaa gtc aac aac aaa gcc ctc cca tcc	826
Lys Gly Lys Gln Phe Thr Cys Lys Val Asn Asn Lys Ala Leu Pro Ser	
245 250 255	
cca atc gag agg acc atc tcc aag gcc aga ggg cag gcc cat caa ccc	874
Pro Ile Glu Arg Thr Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro	
260 265 270	
agt gtg tat gtc ctg ccg cca tcc cgg gag gag ttg agc aag aac aca	922
Ser Val Tyr Val Leu Pro Pro Ser Arg Glu Glu Leu Ser Lys Asn Thr	
275 280 285	
gtc agc ttg aca tgc ctg atc aaa gac ttc ttc cca cct gac att gat	970
Val Ser Leu Thr Cys Leu Ile Lys Asp Phe Phe Pro Pro Asp Ile Asp	
290 295 300	
gtg gag tgg cag agc aat gga cag cag gag cct gag agc aag tac cgc	1018
Val Glu Trp Gln Ser Asn Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg	
305 310 315 320	
acg acc ccg ccc cag ctg gac gag gac ggg tcc tac ttc ctg tac agc	1066
Thr Thr Pro Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser	
325 330 335	

aag ctc tct gtg gac aag agc cgc tgg cag cgg gga gac acc ttc ata 1114  
 Lys Leu Ser Val Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile  
 340 345 350

tgt gcg gtg atg cat gaa gct tta cac aac cac tac aca cag aaa tcc 1162  
 Cys Ala Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
 355 360 365

ctc tcc cat tct ccg ggt aaa tgagcaacac gcccggcacc cagcaagccc 1213  
 Leu Ser His Ser Pro Gly Lys  
 370 375

cccacccttg gctttcagga tcccatgagg atgcctgagc ccccatccct gtgtacataa 1273

ccccgggtag gcacctggca tgaaataaag caccagctac tgccttgga aaaaaaaaaa 1333

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 1364

<210> 32

<211> 375

<212> PRT

<213> Canis familiaris

<400> 32

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys Thr Ser  
 1 5 10 15

Gly Leu Trp Ile Asn Trp Tyr Gly Pro Asn Phe Asp Ser Trp Gly Gln  
 20 25 30

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Thr Ala Pro Ser Val  
 35 40 45

Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser Thr Val Ala  
 50 55 60

Leu Ala Cys Leu Val Ser Gly Tyr Phe Pro Glu Pro Val Thr Val Ser  
 65 70 75 80

Trp Asn Ser Gly Ser Leu Thr Ser Gly Val His Thr Phe Pro Ser Val  
 85 90 95

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Met Val Thr Val Pro  
 100 105 110

Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val Ala His Pro

115								120								125
Ala	Ser	Lys	Thr	Lys	Val	Asp	Lys	Pro	Val	Pro	Lys	Arg	Glu	Asn	Gly	
130						135					140					
Arg	Val	Pro	Arg	Pro	Pro	Asp	Cys	Pro	Lys	Cys	Pro	Thr	Pro	Glu	Met	
145					150					155					160	
Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	
				165					170					175		
Leu	Leu	Ile	Ala	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Leu	
			180					185					190			
Asp	Pro	Glu	Asp	Pro	Glu	Val	Gln	Ile	Ser	Trp	Phe	Val	Asp	Gly	Lys	
		195					200					205				
Gln	Met	Gln	Thr	Ala	Lys	Thr	Gln	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Gly	
210						215					220					
Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Pro	Ile	Gly	His	Gln	Asp	Trp	Leu	
225					230					235					240	
Lys	Gly	Lys	Gln	Phe	Thr	Cys	Lys	Val	Asn	Asn	Lys	Ala	Leu	Pro	Ser	
				245					250					255		
Pro	Ile	Glu	Arg	Thr	Ile	Ser	Lys	Ala	Arg	Gly	Gln	Ala	His	Gln	Pro	
			260					265					270			
Ser	Val	Tyr	Val	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Leu	Ser	Lys	Asn	Thr	
		275					280					285				
Val	Ser	Leu	Thr	Cys	Leu	Ile	Lys	Asp	Phe	Phe	Pro	Pro	Asp	Ile	Asp	
290					295						300					
Val	Glu	Trp	Gln	Ser	Asn	Gly	Gln	Gln	Glu	Pro	Glu	Ser	Lys	Tyr	Arg	
305					310					315					320	
Thr	Thr	Pro	Pro	Gln	Leu	Asp	Glu	Asp	Gly	Ser	Tyr	Phe	Leu	Tyr	Ser	
				325					330					335		
Lys	Leu	Ser	Val	Asp	Lys	Ser	Arg	Trp	Gln	Arg	Gly	Asp	Thr	Phe	Ile	
			340					345					350			
Cys	Ala	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	
		355					360					365				
Leu	Ser	His	Ser	Pro	Gly	Lys										

370

375

<210> 33  
 <211> 1364  
 <212> DNA  
 <213> Canis familiaris

<400> 33  
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 gctttatttc atgccagggtg cctaccgagg gttatgtaca cagggatggg ggctcaggca 120  
 tcctcatggg atcctgaaag ccaaggggtg ggggcttgct ggggtgccggg cgtgttgctc 180  
 atttaccggg agaatgggag agggatttct gtgtgtagtgt gttgtgtaaa gcttcatgca 240  
 tcaccgcaca tatgaagggtg tctccccgct gccagcggct cttgtccaca gagagcttgc 300  
 tgtacaggaa gtaggaccgg tctcgtcca gctggggcgg ggtcgtgcgg tacttgctct 360  
 caggctcctg ctgtccattg ctctgccact ccacatcaat gtcagggtggg aagaagtctt 420  
 tgatcaggca tgtcaagctg actgtgttct tgctcaactc ctcccgggat ggcggcagga 480  
 catacacact ggggttgatgg gcctgccctc tggccttgga gatggctctc tcgattgggg 540  
 atgggagggg tttgttggtg actttgcacg tgaactgctt ccccttgagc cagtcttggt 600  
 gcccaatggg gaggacactg accacacggg aggtgccatt gaactgctcc tcacgaggct 660  
 gagtcttggc tgtttgcatc tgcttaccgt ccacgaacca gctgatctgc acctcagggt 720  
 cttctgggtc cagatccacc accacacatg tgacctcagg tgttcgggca atcaagaggg 780  
 tgtccttggg tttcggggga aagatgaaga ccgaaggccc tcccagcatt tcaggggttg 840  
 ggcatttggg acaatcagggt gggcgaggaa ctcttccatt ttctcttttg ggcactggct 900  
 tgtctacttt agttttgctg gccgggtggg ccacgttgca ggtgaagggtc tcgctgggccc 960  
 acctgctgga gggcactgtc accatgctgc tgaggagta gagccctgag gactgcagga 1020  
 cggacgggaa ggtgtgcaca ccgctgggtc aggagccgga attccaggac acagttacag 1080  
 gctcggggaa gtagcctgac accaggcagg ccaggggccac cgtggagccg gaagtggacc 1140  
 cgcagctggg ggccagtggg aaaaccgagg gggccgtggt ggaggctgag gagacggtga 1200  
 ccagggttcc ctggccccag gagtcaaaat tcggaccgta ccagttgatc cataaccac 1260  
 ttgtacagta atacagggcc gtatcctcag ctctcagggt gttcatctgc agatacagcg 1320  
 tgttctcgac attgtctctg gaaatgggtga atcggcctcg tgcc 1364

<210> 34  
 <211> 1168  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> CDS  
 <222> (48) .. (1166)

<400> 34  
 ccagggtgacc ccattcagtg ctcaggacac aacacagaca aaccacc atg gag tct 56  
 Met Glu Ser

1

gtg ctc tgc tgg gtt ttc ctt gtc tct att tta aaa ggt gtc cag ggt	104
Val Leu Cys Trp Val Phe Leu Val Ser Ile Leu Lys Gly Val Gln Gly	
5 10 15	
 gag gtg caa ctg gtg gag tct ggg gga gac ctg gtg aag cct ggg ggg	152
Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys Pro Gly Gly	
20 25 30 35	
 tcc ttg aga ctg tcc tgt gtg gcc tct gga ttc acc ttc agt gac tat	200
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Asp Tyr	
40 45 50	
 ggc atg agt tgg gtc cgt cag tct cca ggg aag ggg ctg cag tgg gtc	248
Gly Met Ser Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Gln Trp Val	
55 60 65	
 gca gct gtt agc aat cgt gga gat act tac tac gca gac gct gtg aag	296
Ala Ala Val Ser Asn Arg Gly Asp Thr Tyr Tyr Ala Asp Ala Val Lys	
70 75 80	
 ggc cga ttc acc atc tcc aga gac aac gcc aag aac acg ctg tat ctc	344
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu	
85 90 95	
 cag atg agc agc ctg aaa gcc gag gac acg gca atc tat cac tgt gtg	392
Gln Met Ser Ser Leu Lys Ala Glu Asp Thr Ala Ile Tyr His Cys Val	
100 105 110 115	
 acg gga gta tgg ccg cga cat tat tat ggt atg gac cac tgg ggc aat	440
Thr Gly Val Trp Pro Arg His Tyr Tyr Gly Met Asp His Trp Gly Asn	
120 125 130	
 ggc acc tca ctc ttc gtg tcc tca gcc tcc acc acg gcc ccc tcg gtt	488
Gly Thr Ser Leu Phe Val Ser Ser Ala Ser Thr Thr Ala Pro Ser Val	
135 140 145	
 ttc cca ctg gcc ccc agc tgc ggg tcc act tcc ggc tcc acg gtg gcc	536
Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser Thr Val Ala	
150 155 160	
 ctg gcc tgc ctg gtg tca ggc tac ttc ccc gag cct gta act gtg tcc	584
Leu Ala Cys Leu Val Ser Gly Tyr Phe Pro Glu Pro Val Thr Val Ser	
165 170 175	
 tgg aat tcc ggc tcc ttg acc agc ggt gtg cac acc ttc ccg tcc gtc	632
Trp Asn Ser Gly Ser Leu Thr Ser Gly Val His Thr Phe Pro Ser Val	
180 185 190 195	

ctg cag tcc tca ggg ctc tac tcc ctc agc agc acg gtg aca gtg ccc	680
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Thr Val Thr Val Pro	
200 205 210	
tcc agc agg tgg ccc agc gag acc ttc acc tgc aac gtg gtc cac ccg	728
Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val Val His Pro	
215 220 225	
gcc agc aac act aaa gta gac aag cca gtg ccc aaa gag tcc acc tgc	776
Ala Ser Asn Thr Lys Val Asp Lys Pro Val Pro Lys Glu Ser Thr Cys	
230 235 240	
aag tgt ata tcc cca tgc cca gtc cct gaa tca ctg gga ggg cct tcg	824
Lys Cys Ile Ser Pro Cys Pro Val Pro Glu Ser Leu Gly Gly Pro Ser	
245 250 255	
gtc ttc atc ttt ccc ccg aaa ccc aag gac atc ctc agg att acc cga	872
Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg Ile Thr Arg	
260 265 270 275	
aca ccc gag atc acc tgt gtg gtg tta gat ctg ggc cgt gag gac cct	920
Thr Pro Glu Ile Thr Cys Val Val Leu Asp Leu Gly Arg Glu Asp Pro	
280 285 290	
gag gtg cag atc agc tgg ttc gtg gat ggt aag gag gtg cac aca gcc	968
Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val His Thr Ala	
295 300 305	
aag acg cag cct cgt gag cag cag ttc aac agc acc tac cgt gtg gtc	1016
Lys Thr Gln Pro Arg Glu Gln Gln Phe Asn Ser Thr Tyr Arg Val Val	
310 315 320	
agc gtc ctc ccc att gag cac cag gac tgg ctc acc gga aag gag ttc	1064
Ser Val Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly Lys Glu Phe	
325 330 335	
aag tgc aga gtc aac cac ata ggc ccc ccg tcc ccc atc gag agg act	1112
Lys Cys Arg Val Asn His Ile Gly Pro Pro Ser Pro Ile Glu Arg Thr	
340 345 350 355	
atc tcc aaa gcc aga ggg caa gcc cat cag ccc agt gtg tat gtc ctg	1160
Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val Tyr Val Leu	
360 365 370	
ccg cca tc	1168
Pro Pro	



<210> 35  
 <211> 373  
 <212> PRT  
 <213> Canis familiaris  
  
 <400> 35  
 Met Glu Ser Val Leu Cys Trp Val Phe Leu Val Ser Ile Leu Lys Gly  
   1                  5                  10                  15  
  
 Val Gln Gly Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys  
                   20                  25                  30  
  
 Pro Gly Gly Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe  
           35                  40                  45  
  
 Ser Asp Tyr Gly Met Ser Trp Val Arg Gln Ser Pro Gly Lys Gly Leu  
       50                  55                  60  
  
 Gln Trp Val Ala Ala Val Ser Asn Arg Gly Asp Thr Tyr Tyr Ala Asp  
   65                  70                  75                  80  
  
 Ala Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr  
                   85                  90                  95  
  
 Leu Tyr Leu Gln Met Ser Ser Leu Lys Ala Glu Asp Thr Ala Ile Tyr  
           100                  105                  110  
  
 His Cys Val Thr Gly Val Trp Pro Arg His Tyr Tyr Gly Met Asp His  
       115                  120                  125  
  
 Trp Gly Asn Gly Thr Ser Leu Phe Val Ser Ser Ala Ser Thr Thr Ala  
       130                  135                  140  
  
 Pro Ser Val Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser  
   145                  150                  155                  160  
  
 Thr Val Ala Leu Ala Cys Leu Val Ser Gly Tyr Phe Pro Glu Pro Val  
                   165                  170                  175  
  
 Thr Val Ser Trp Asn Ser Gly Ser Leu Thr Ser Gly Val His Thr Phe  
           180                  185                  190  
  
 Pro Ser Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Thr Val  
       195                  200                  205  
  
 Thr Val Pro Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val  
       210                  215                  220

Val His Pro Ala Ser Asn Thr Lys Val Asp Lys Pro Val Pro Lys Glu  
225 230 235 240

Ser Thr Cys Lys Cys Ile Ser Pro Cys Pro Val Pro Glu Ser Leu Gly  
245 250 255

Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg  
260 265 270

Ile Thr Arg Thr Pro Glu Ile Thr Cys Val Val Leu Asp Leu Gly Arg  
275 280 285

Glu Asp Pro Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val  
290 295 300

His Thr Ala Lys Thr Gln Pro Arg Glu Gln Gln Phe Asn Ser Thr Tyr  
305 310 315 320

Arg Val Val Ser Val Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly  
325 330 335

Lys Glu Phe Lys Cys Arg Val Asn His Ile Gly Pro Pro Ser Pro Ile  
340 345 350

Glu Arg Thr Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val  
355 360 365

Tyr Val Leu Pro Pro  
370

<210> 36

<211> 1168

<212> DNA

<213> Canis familiaris

<400> 36

gatggcggca ggacatacac actgggctga tgggcttgcc ctctggcttt ggagatagtc 60  
ctctcgatgg gggacggggg gcctatgtgg ttgactctgc acttgaactc ctttccggtg 120  
agccagtcct ggtgctcaat ggggaggacg ctgaccacac ggtaggtgct gttgaactgc 180  
tgctcacgag gctgctcctt ggctgtgtgc acctccttac catccacgaa ccagctgatc 240  
tgcacctcag ggtcctcacg gccagatct aacaccacac aggtgatctc ggggtgttcgg 300  
gtaatcctga ggatgtcctt gggtttcggg ggaaagatga agaccgaagg ccctcccagt 360  
gattcaggga ctgggcatgg ggatatacac ttgcagggtg actctttggg cactggcttg 420  
tctacttttag tggtgctggc cgggtggacc acgttgcagg tgaaggtctc gctggggccac 480  
ctgctggagg gcactgtcac cgtgctgctg agggagtaga gccctgagga ctgcaggacg 540

gacgggaagg tgtgcacacc gctgggtcaag gagccggaat tccaggacac agttacaggc 600  
tcggggaagt agcctgacac caggcaggcc agggccaccg tggagccgga agtggaccgc 660  
cagctggggg ccagtgggaa aaccgagggg gccgtgggtg aggctgagga cacgaagagt 720  
gaggtgccat tgccccagtg gtccatacca taataatgtc gcggccatac tcccgtcaca 780  
cagtgataga ttgccgtgtc ctccgctttc aggtctgtca tctggagata cagcgtgttc 840  
ttggcgttgt ctctggagat ggtgaatcgg ccccttcacag cgtctgcgta gtaagtatct 900  
ccacgattgc taacagctgc gaccactgc agccccttcc ctggagactg acggacccaa 960  
ctcatgccat agtcaactgaa ggtgaatcca gaggccacac aggacagtct caaggacccc 1020  
ccaggcttca ccaggctctcc cccagactcc accagttgca cctcaccctg gacacctttt 1080  
aaaatagaga caagggaaac ccagcagagc acagactcca tgggtggttg tctgtgttgt 1140  
gtcctgagca ctgaatgggg tcacctgg 1168

<210> 37

<211> 1059

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (1)..(1056)

<400> 37

tgg ccg cga cat tat tat ggt atg gac cac tgg ggc aat ggc acc tca 48  
Trp Pro Arg His Tyr Tyr Gly Met Asp His Trp Gly Asn Gly Thr Ser  
1 5 10 15

ctc ttc gtg tcc tca gcc tcc acc acg gcc ccc tcg gtt ttc cca ctg 96  
Leu Phe Val Ser Ser Ala Ser Thr Thr Ala Pro Ser Val Phe Pro Leu  
20 25 30

gcc ccc agc tgc ggg tcc act tcc ggc tcc acg gtg gcc ctg gcc tgc 144  
Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser Thr Val Ala Leu Ala Cys  
35 40 45

ctg gtg tca ggc tac ttc ccc gag cct gta act gtg tcc tgg aat tcc 192  
Leu Val Ser Gly Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser  
50 55 60

gac tcc ttg acc agc ggt gtg cac acc ttc ccg tcc gtc ctg cag tcc 240  
Asp Ser Leu Thr Ser Gly Val His Thr Phe Pro Ser Val Leu Gln Ser  
65 70 75 80

tca ggg ctc tac tcc ctc agc agc acg gtg aca gtg ccc tcc agc agg 288  
Ser Gly Leu Tyr Ser Leu Ser Ser Thr Val Thr Val Pro Ser Ser Arg  
85 90 95

tgg ccc agc gag acc ttc acc tgc aac gtg gtc cac ccg gcc agc aac 336

Trp	Pro	Ser	Glu	Thr	Phe	Thr	Cys	Asn	Val	Val	His	Pro	Ala	Ser	Asn		
			100					105					110				
act	aaa	gta	gac	aag	cca	gtg	ccc	aaa	gag	tcc	acc	tgc	aag	tgt	ata	384	
Thr	Lys	Val	Asp	Lys	Pro	Val	Pro	Lys	Glu	Ser	Thr	Cys	Lys	Cys	Ile		
		115						120				125					
tcc	cca	tgc	cca	gtc	cct	gaa	tca	ctg	gga	ggg	cct	tcg	gtc	ttc	atc	432	
Ser	Pro	Cys	Pro	Val	Pro	Glu	Ser	Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile		
		130						135				140					
ttt	ccc	ccg	aaa	ccc	aag	gac	atc	ctc	agg	att	acc	cga	aca	ccc	gag	480	
Phe	Pro	Pro	Lys	Pro	Lys	Asp	Ile	Leu	Arg	Ile	Thr	Arg	Thr	Pro	Glu		
145						150				155					160		
atc	acc	tgt	gtg	gtg	tta	gat	ctg	ggc	cgt	gag	gac	cct	gag	gtg	cag	528	
Ile	Thr	Cys	Val	Val	Leu	Asp	Leu	Gly	Arg	Glu	Asp	Pro	Glu	Val	Gln		
				165					170					175			
atc	agc	tgg	ttc	gtg	gat	ggt	aag	gag	gtg	cac	aca	gcc	aag	acg	cag	576	
Ile	Ser	Trp	Phe	Val	Asp	Gly	Lys	Glu	Val	His	Thr	Ala	Lys	Thr	Gln		
			180						185					190			
cct	cgt	gag	cag	cag	ttc	aac	agc	acc	tac	cgt	gtg	gtc	agc	gtc	ctc	624	
Pro	Arg	Glu	Gln	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu		
			195						200					205			
ccc	att	gag	cac	cag	gac	tgg	ctc	acc	gga	aag	gag	ttc	aag	tgc	aga	672	
Pro	Ile	Glu	His	Gln	Asp	Trp	Leu	Thr	Gly	Lys	Glu	Phe	Lys	Cys	Arg		
		210					215					220					
gtc	aac	cac	ata	ggc	ctc	ccg	tcc	ccc	atc	gag	agg	act	atc	tcc	aaa	720	
Val	Asn	His	Ile	Gly	Leu	Pro	Ser	Pro	Ile	Glu	Arg	Thr	Ile	Ser	Lys		
225					230					235					240		
gcc	aga	ggg	caa	gcc	cat	cag	ccc	agt	gtg	tat	gtc	ctg	cca	cca	tcc	768	
Ala	Arg	Gly	Gln	Ala	His	Gln	Pro	Ser	Val	Tyr	Val	Leu	Pro	Pro	Ser		
				245						250					255		
cca	aag	gag	ttg	tca	tcc	agt	gac	acg	gtc	acc	ctg	acc	tgc	ctg	atc	816	
Pro	Lys	Glu	Leu	Ser	Ser	Ser	Asp	Thr	Val	Thr	Leu	Thr	Cys	Leu	Ile		
			260						265					270			
aaa	gac	ttc	ttc	cca	cct	gag	att	gat	gtg	gag	tgg	cag	agc	aat	gga	864	
Lys	Asp	Phe	Phe	Pro	Pro	Glu	Ile	Asp	Val	Glu	Trp	Gln	Ser	Asn	Gly		
		275						280						285			
cag	ccg	gag	ccc	gag	agc	aag	tac	cac	acg	act	gcg	ccc	cag	ctg	gac	912	

Gln Pro Glu Pro Glu Ser Lys Tyr His Thr Thr Ala Pro Gln Leu Asp  
 290 295 300

gag gac ggg tcc tac ttc ctg tac agc aag ctc tct gtg gac aag agc 960  
 Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys Ser  
 305 310 315 320

cgc tgg cag cag gga gac ccc ttc aca tgt gcg gtg atg cat gaa gct 1008  
 Arg Trp Gln Gln Gly Asp Pro Phe Thr Cys Ala Val Met His Glu Ala  
 325 330 335

cta cag aac cac tac aca gat cta tcc ctc tcc cat tct ccg ggt aaa 1056  
 Leu Gln Asn His Tyr Thr Asp Leu Ser Leu Ser His Ser Pro Gly Lys  
 340 345 350

tga 1059

<210> 38

<211> 352

<212> PRT

<213> Canis familiaris

<400> 38

Trp Pro Arg His Tyr Tyr Gly Met Asp His Trp Gly Asn Gly Thr Ser  
 1 5 10 15

Leu Phe Val Ser Ser Ala Ser Thr Thr Ala Pro Ser Val Phe Pro Leu  
 20 25 30

Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser Thr Val Ala Leu Ala Cys  
 35 40 45

Leu Val Ser Gly Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser  
 50 55 60

Asp Ser Leu Thr Ser Gly Val His Thr Phe Pro Ser Val Leu Gln Ser  
 65 70 75 80

Ser Gly Leu Tyr Ser Leu Ser Ser Thr Val Thr Val Pro Ser Ser Arg  
 85 90 95

Trp Pro Ser Glu Thr Phe Thr Cys Asn Val Val His Pro Ala Ser Asn  
 100 105 110

Thr Lys Val Asp Lys Pro Val Pro Lys Glu Ser Thr Cys Lys Cys Ile  
 115 120 125

Ser Pro Cys Pro Val Pro Glu Ser Leu Gly Gly Pro Ser Val Phe Ile  
 130 135 140  
 Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg Ile Thr Arg Thr Pro Glu  
 145 150 155 160  
 Ile Thr Cys Val Val Leu Asp Leu Gly Arg Glu Asp Pro Glu Val Gln  
 165 170 175  
 Ile Ser Trp Phe Val Asp Gly Lys Glu Val His Thr Ala Lys Thr Gln  
 180 185 190  
 Pro Arg Glu Gln Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu  
 195 200 205  
 Pro Ile Glu His Gln Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys Arg  
 210 215 220  
 Val Asn His Ile Gly Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser Lys  
 225 230 235 240  
 Ala Arg Gly Gln Ala His Gln Pro Ser Val Tyr Val Leu Pro Pro Ser  
 245 250 255  
 Pro Lys Glu Leu Ser Ser Ser Asp Thr Val Thr Leu Thr Cys Leu Ile  
 260 265 270  
 Lys Asp Phe Phe Pro Pro Glu Ile Asp Val Glu Trp Gln Ser Asn Gly  
 275 280 285  
 Gln Pro Glu Pro Glu Ser Lys Tyr His Thr Thr Ala Pro Gln Leu Asp  
 290 295 300  
 Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys Ser  
 305 310 315 320  
 Arg Trp Gln Gln Gly Asp Pro Phe Thr Cys Ala Val Met His Glu Ala  
 325 330 335  
 Leu Gln Asn His Tyr Thr Asp Leu Ser Leu Ser His Ser Pro Gly Lys  
 340 345 350

<210> 39

<211> 1059

<212> DNA

<213> Canis familiaris

<400> 39  
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 catcaccgca catgtgaagg ggtctccctg ctgccagcgg ctcttggtcca cagagagctt 120  
 gctgtacagg aagtaggacc cgtcctcgtc cagctggggc gcagtcgtgt ggtacttgct 180  
 ctcgggctcc ggctgtccat tgctctgcca ctccacatca atctcaggtg ggaagaagtc 240  
 tttgatcagg caggtcaggg tgaccgtgtc actggatgac aactcctttg gggatggtgg 300  
 caggacatac aactgggct gatgggcttg cctctggct ttggagatag tcctctcgat 360  
 gggggacggg aggcctatgt ggttgactct gcaattgaac tcctttccgg tgagccagtc 420  
 ctggtgctca atggggagga cgctgaccac acggtaggtg ctggtgaact gctgctcacg 480  
 aggctgcgtc ttggctgtgt gcacctcctt accatccacg aaccagctga tctgcacctc 540  
 agggctcctc cggcccagat ctaacaccac acaggtgatc tcgggtgttc gggtaatcct 600  
 gaggatgtcc ttgggtttcg ggggaaagat gaagaccgaa ggccctccca gtgattcagg 660  
 gactgggcat ggggatatac acttgacagg ggactctttg ggcactggct tgtctacttt 720  
 agtggtgctg gccgggtgga ccacgttgca ggtgaaggtc tcgctgggcc acctgctgga 780  
 gggcactgtc accgtgctgc tgagggagta gagccctgag gactgcagga cggacgggaa 840  
 ggtgtgcaca ccgtggtca aggagtcgga attccaggac acagttacag gctcggggaa 900  
 gtagcctgac accaggcagg ccagggccac cgtggagccg gaagtggacc cgcagctggg 960  
 ggccagtggg aaaaccgagg gggccgtggt ggaggctgag gacacgaaga gtgaggtgcc 1020  
 attgccccag tggtcatac cataataatg tcgcgcca 1059

<210> 40

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 Primer

<220>

<221> misc\_feature

<222> (15)

<223> At position 15, n = unknown

<220>

<221> misc\_feature

<222> (21)

<223> At position 21, n = unknown

<400> 40

caycargayt ggytnaaygg naargartty aartgy 36

<210> 41

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 41

gccctccagc aggtggccca gcgagacc

28

<210> 42

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 42

ggggatggcg gcaggacata cac

23

<210> 43

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 43

tttaccgga gaatgggaga ggg

23

<210> 44

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 44

ggtctgcgtg ggccacctgc tggagggc

28



<210> 45  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 45  
gggtgggggg cttgctgggt gccgggcg 28

<210> 46  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 46  
ccaggtgacc ccattcagtg ctcaggacac 30

<210> 47  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 47  
ctgtgtgacg ggagtatggc cgcgac 26

<210> 48  
<211> 483  
<212> DNA  
<213> Canis familiaris

<220>  
<221> misc\_feature  
<222> (470)

<223> At position 470, n = unknown

<400> 48

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agtcatttttg acaacaaaca ggataagaaa attgctcctg aaactcatcg ttcaaaagaa 120
gtacccttga atgagaggat ttgtctgcaa gtgggggtccc agtgcagcac caatgaaagt 180
gacaatccta gcatttttggg ggaaaagtgc accccaccac ctgaaggtgg tcctgagtcg 240
gctgtgactg agctacaatg tgtttggcac aacctgagct acatgaagtg tacttggctt 300
cctggaagga atacaagccc tgacaccaac tatactctct actattggca cagcagcctg 360
ggaaaaattc ttcaatgcga agacatctat agagaaggtc aacacattgg ttgttccttt 420
gctctgacta atttgaagga ttccagtttt gaacaacaca gtgtccagan gatgggtcaag 480
ggt 483
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<210> 49

<211> 1547

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (1)..(1215)

<400> 49

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Gly Gly Val Ala Ala Pro Thr Glu Thr Gln Pro Pro Val Thr Asn Leu
  1          5          10          15

agt gtt tct gtt gaa aac ctc tgc acg gtc ata tgg aca tgg aac cct 96
Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile Trp Thr Trp Asn Pro
      20          25          30

ccc gag gga gcc agc ccg aat tgc acc tta cgg tat ttt agt cat ttt 144
Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg Tyr Phe Ser His Phe
      35          40          45

gac aac aaa cag gat aag aaa att gct cct gaa act cat cgt tca aaa 192
Asp Asn Lys Gln Asp Lys Lys Ile Ala Pro Glu Thr His Arg Ser Lys
      50          55          60

gaa gta ccc ctg aat gag agg att tgt ctg caa gtg ggg tcc cag tgc 240
Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln Val Gly Ser Gln Cys
      65          70          75          80

agc acc aat gaa agt gac aat cct agc att ttg gtg gaa aag tgc acc 288
Ser Thr Asn Glu Ser Asp Asn Pro Ser Ile Leu Val Glu Lys Cys Thr
      85          90          95
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cca cca cct gaa ggt gat cct gag tcg gct gtg act gag cta caa tgt	336
Pro Pro Pro Glu Gly Asp Pro Glu Ser Ala Val Thr Glu Leu Gln Cys	
100 105 110	
gtt tgg cac aac ctg agc tac atg aag tgt act tgg ctt cct gga agg	384
Val Trp His Asn Leu Ser Tyr Met Lys Cys Thr Trp Leu Pro Gly Arg	
115 120 125	
aat aca agc cct gac acc aac tat act ctc tac tat tgg cac agc agc	432
Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr Tyr Trp His Ser Ser	
130 135 140	
ctg gga aaa att ctt caa tgc gaa gac atc tat aga gaa ggt caa cac	480
Leu Gly Lys Ile Leu Gln Cys Glu Asp Ile Tyr Arg Glu Gly Gln His	
145 150 155 160	
att ggt tgt tcc ttt gct ctg act aat ttg aag gat tcc agt ttt gaa	528
Ile Gly Cys Ser Phe Ala Leu Thr Asn Leu Lys Asp Ser Ser Phe Glu	
165 170 175	
caa cac agt gtc caa ata atg gtc aag gat aat gca aga aaa att aga	576
Gln His Ser Val Gln Ile Met Val Lys Asp Asn Ala Arg Lys Ile Arg	
180 185 190	
ccg tcc ttc aat ata gtg cct tta act tct cat gtg aaa cct gat ccc	624
Pro Ser Phe Asn Ile Val Pro Leu Thr Ser His Val Lys Pro Asp Pro	
195 200 205	
ccc cat att aag cgt ctc ttc ttc caa aat ggt aac ttg tat gtg caa	672
Pro His Ile Lys Arg Leu Phe Phe Gln Asn Gly Asn Leu Tyr Val Gln	
210 215 220	
tgg aag aat cca caa aat ttt tat agc aga tgc tta tct tac caa gta	720
Trp Lys Asn Pro Gln Asn Phe Tyr Ser Arg Cys Leu Ser Tyr Gln Val	
225 230 235 240	
gaa gtc aat aac agc cag act gag acg aat gat ata ttc tac gtt gaa	768
Glu Val Asn Asn Ser Gln Thr Glu Thr Asn Asp Ile Phe Tyr Val Glu	
245 250 255	
gaa gcc aaa tgt cag aat tca gaa ttt gag gga aac ctg gag ggt aca	816
Glu Ala Lys Cys Gln Asn Ser Glu Phe Glu Gly Asn Leu Glu Gly Thr	
260 265 270	
att tgt ttc atg gtc ccc ggc gtt ctt cct gat act ttg aac aca gtc	864
Ile Cys Phe Met Val Pro Gly Val Leu Pro Asp Thr Leu Asn Thr Val	
275 280 285	

aga ata aga gtc aga aca aat aag tta tgc tat gag gat gac aaa ctc 912  
 Arg Ile Arg Val Arg Thr Asn Lys Leu Cys Tyr Glu Asp Asp Lys Leu  
 290 295 300

tgg agt aat tgg agt caa gcg atg agt ata ggt gag aat acc gac ccc 960  
 Trp Ser Asn Trp Ser Gln Ala Met Ser Ile Gly Glu Asn Thr Asp Pro  
 305 310 315 320

acg ttc tat ata acc atg ttg ctc gcc act caa gtc atc gtt gca ggt 1008  
 Thr Phe Tyr Ile Thr Met Leu Leu Ala Thr Gln Val Ile Val Ala Gly  
 325 330 335

gcc atc ata atc ctt ctg ctt tat ctc aaa agg ctc aag atc att ata 1056  
 Ala Ile Ile Ile Leu Leu Leu Tyr Leu Lys Arg Leu Lys Ile Ile Ile  
 340 345 350

ttc cct cca att cct gat cct ggc aag att ttt aaa gaa atg ttt gga 1104  
 Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe Lys Glu Met Phe Gly  
 355 360 365

gac cag aat gat gat acg ctg cac tgg agg aag tac gac atc tat gag 1152  
 Asp Gln Asn Asp Asp Thr Leu His Trp Arg Lys Tyr Asp Ile Tyr Glu  
 370 375 380

aag caa aca aaa gaa gaa acg gac tca gta gtg ctg att gaa aac ctg 1200  
 Lys Gln Thr Lys Glu Glu Thr Asp Ser Val Val Leu Ile Glu Asn Leu  
 385 390 395 400

aag aaa gcc tct cag taatggggat aacttatttt agccttcagc atgaccttgt 1255  
 Lys Lys Ala Ser Gln  
 405

aaagattcat cccacgttc tcgggaagct tcaagggtcaa gcatcttggg aaaggacatt 1315

acagtttcta cagcatggtg tacctgggca tctccgacta cttcttcaac acagcagggc 1375

ttgtgtacca agaggcaggg gccttaaaca tgaccatcac ggacgacatg ataccaaaga 1435

aatccaaatt ccgactgaca accgattttt tggggaccct cataccccaa gtggccgaga 1495

tgttccccaa catgacggtt caattcaacg tctgggcctc ctccccgccg ca 1547

<210> 50  
 <211> 405  
 <212> PRT  
 <213> Canis familiaris

<400> 50

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Ser	Val	Ser	Val	Glu	Asn	Leu	Cys	Thr	Val	Ile	Trp	Thr	Trp	Asn	Pro	20	25	30	
Pro	Glu	Gly	Ala	Ser	Pro	Asn	Cys	Thr	Leu	Arg	Tyr	Phe	Ser	His	Phe	35	40	45	
Asp	Asn	Lys	Gln	Asp	Lys	Lys	Ile	Ala	Pro	Glu	Thr	His	Arg	Ser	Lys	50	55	60	
Glu	Val	Pro	Leu	Asn	Glu	Arg	Ile	Cys	Leu	Gln	Val	Gly	Ser	Gln	Cys	65	70	75	80
Ser	Thr	Asn	Glu	Ser	Asp	Asn	Pro	Ser	Ile	Leu	Val	Glu	Lys	Cys	Thr	85	90	95	
Pro	Pro	Pro	Glu	Gly	Asp	Pro	Glu	Ser	Ala	Val	Thr	Glu	Leu	Gln	Cys	100	105	110	
Val	Trp	His	Asn	Leu	Ser	Tyr	Met	Lys	Cys	Thr	Trp	Leu	Pro	Gly	Arg	115	120	125	
Asn	Thr	Ser	Pro	Asp	Thr	Asn	Tyr	Thr	Leu	Tyr	Tyr	Trp	His	Ser	Ser	130	135	140	
Leu	Gly	Lys	Ile	Leu	Gln	Cys	Glu	Asp	Ile	Tyr	Arg	Glu	Gly	Gln	His	145	150	155	160
Ile	Gly	Cys	Ser	Phe	Ala	Leu	Thr	Asn	Leu	Lys	Asp	Ser	Ser	Phe	Glu	165	170	175	
Gln	His	Ser	Val	Gln	Ile	Met	Val	Lys	Asp	Asn	Ala	Arg	Lys	Ile	Arg	180	185	190	
Pro	Ser	Phe	Asn	Ile	Val	Pro	Leu	Thr	Ser	His	Val	Lys	Pro	Asp	Pro	195	200	205	
Pro	His	Ile	Lys	Arg	Leu	Phe	Phe	Gln	Asn	Gly	Asn	Leu	Tyr	Val	Gln	210	215	220	
Trp	Lys	Asn	Pro	Gln	Asn	Phe	Tyr	Ser	Arg	Cys	Leu	Ser	Tyr	Gln	Val	225	230	235	240
Glu	Val	Asn	Asn	Ser	Gln	Thr	Glu	Thr	Asn	Asp	Ile	Phe	Tyr	Val	Glu	245	250	255	

Glu Ala Lys Cys Gln Asn Ser Glu Phe Glu Gly Asn Leu Glu Gly Thr  
                   260                                  265                                  270  
 Ile Cys Phe Met Val Pro Gly Val Leu Pro Asp Thr Leu Asn Thr Val  
                   275                                  280                                  285  
 Arg Ile Arg Val Arg Thr Asn Lys Leu Cys Tyr Glu Asp Asp Lys Leu  
                   290                                  295                                  300  
 Trp Ser Asn Trp Ser Gln Ala Met Ser Ile Gly Glu Asn Thr Asp Pro  
 305                                  310                                  315                                  320  
 Thr Phe Tyr Ile Thr Met Leu Leu Ala Thr Gln Val Ile Val Ala Gly  
                                   325                                  330                                  335  
 Ala Ile Ile Ile Leu Leu Leu Tyr Leu Lys Arg Leu Lys Ile Ile Ile  
                   340                                  345                                  350  
 Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe Lys Glu Met Phe Gly  
                   355                                  360                                  365  
 Asp Gln Asn Asp Asp Thr Leu His Trp Arg Lys Tyr Asp Ile Tyr Glu  
                   370                                  375                                  380  
 Lys Gln Thr Lys Glu Glu Thr Asp Ser Val Val Leu Ile Glu Asn Leu  
 385                                  390                                  395                                  400  
 Lys Lys Ala Ser Gln  
                                   405

<210> 51  
 <211> 1547  
 <212> DNA  
 <213> Canis familiaris

<400> 51  
 tgcggcgggg aggaggccca gacgttgaat tgaaccgtca tgttggggaa catctcggcc 60  
 acttggggta tgagggtccc caaaaaatcg gttgtcagtc ggaatttgga tttctttggt 120  
 atcatgtcgt ccgtgatggt catgtttaag gccctgcct cttggtacac aagccctgct 180  
 gtgttgaaga agtagtcgga gatgccagg tacaccatgc tgtagaaact gtaatgtcct 240  
 ttccaagat gcttgacctt gaagcttccc gagaacgtgg ggatgaatct ttacaaggctc 300  
 atgctgaagg ctaaaataag ttatcccat tactgagagg ctttcttcag gttttcaatc 360  
 agcactactg agtccgtttc ttcttttggt tgcttctcat agatgtcgta cttcctccag 420  
 tgcagcgtat catcattctg gtctccaaac atttctttaa aaatcttgcc aggatcagga 480  
 attggaggga atataatgat cttgagcctt ttgagataaa gcagaaggat tatgatggca 540

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cctgcaacga tgacttgagt ggcgagcaac atgggttatat agaacgtggg gtcggtattc 600
tcacctatac tcacgccttg actccaatta ctccagagtt tgtcatcctc atagcataac 660
ttatttggtt tgactcttat tctgactgtg ttcaaagtat caggaagaac gccgggggacc 720
atgaaacaaa ttgtaccctc cagggtttccc tcaaattctg aattctgaca tttggcttct 780
tcaacgtaga atatatcatt cgtctcagtc tggctgttat tgacttctac ttggtaagat 840
aagcatctgc tataaaaatt ttgtggattc ttccattgca catacaagtt accatttttg 900
aagaagagac gcttaatatg ggggggatca ggtttcacat gagaagttaa aggcactata 960
ttgaaggacg gtctaatttt tcttgcatca tccttgacca ttatttgga actgtgttgt 1020
tcaaaactgg aatccttcaa attagtcaga gcaaaggaac aaccaatgtg ttgaccttct 1080
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tagttggtgt cagggttctg attccttcca ggaagccaag tacacttcat gtagctcagg 1200
ttgtgcaaaa cacattgtag ctcaagtcaca gccgactcag gatcaccttc aggtggtggg 1260
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acttgacagc aaatcctctc attcaggggt acttcttttg aacgatgagt ttcaggagca 1380
atcttcttat cctgtttgtt gtcaaaatga ctaaaatacc gtaagggtgca attcgggctg 1440
gctccctcgg gaggggtcca tgtccatatg accgtgcaga ggttttcaac agaaacactc 1500
aaattcgtca cagggtggctg agtttcgggtg ggtgcgccga ccccgcc 1547

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<210> 52

<211> 1215

<212> DNA

<213> *Canis familiaris*

<400> 52

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gaaaacctct gcacggctcat atggacatgg aacctcccg agggagccag cccgaattgc 120
accttacggg atttttagtca ttttgacaac aaacaggata agaaaattgc tcctgaaact 180
catcgttcaa aagaagtacc cctgaatgag aggatttgtc tgcaagtggg gtcccagtcg 240
agcaccaatg aaagtgacaa tcctagcatt ttggtggaaa agtgcacccc accacctgaa 300
ggtgatcctg agtcggctgt gactgagcta caatgtgttt ggcacaacct gagctacatg 360
aagtgtactt ggcttccttg aaggaatata agccctgaca ccaactatac tctctactat 420
tggcacagca gcctgggaaa aattcttcaa tgcaagaca tctatagaga aggtcaacac 480
attggttggt cctttgctct gactaatttg aaggattcca gttttgaaca acacagtgtc 540
caaataatgg tcaaggataa tgcaagaaaa attagaccgt ccttcaatat agtgccttta 600
acttctcatg tgaaacctga tcccccccat attaaagctc tcttcttcca aaatggtaac 660
ttgtatgtgc aatggaagaa tccacaaaat ttttatagca gatgcttatc ttaccaagta 720
gaagtcaata acagccagac tgagacgaat gatataattc acgttgaaga agccaaatgt 780
cagaattcag aatttgaggg aaacctggag ggtacaattt gtttcatggt ccccggtgtt 840
cttcctgata ctttgaacac agtcagaata agagtcagaa caaataagtt atgctatgag 900
gatgacaaac tctggagtaa ttggagtcaa gcatgagta taggtgagaa taccgacccc 960
acgttctata taacctgtt gctcgccact caagtcacg ttgcagggtc catcataatc 1020
cttctgcttt atctcaaaag gctcaagatc attatattcc ctccaattcc tgatcctggc 1080
aagattttta aagaaatgtt tggagaccag aatgatgata cgctgcactg gaggaagtac 1140
gacatctatg agaagcaaac aaaagaagaa acggactcag tagtgctgat tgaaaacctg 1200
aagaaagcct ctacg 1215

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<210> 53  
 <211> 1215  
 <212> DNA  
 <213> Canis familiaris

<400> 53  
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 ttcttttaaa atcttgccag gatcaggaat tggagggaat ataatgatct tgagcctttt 180  
 gagataaagc agaaggatta tgatggcacc tgcaacgatg acttgagtgg cgagcaacat 240  
 ggttatatag aacgtggggg cgggtattct acctatactc atcgcttgac tccaattact 300  
 ccagagtttg tcatcctcat agcataactt atttgttctg actcttattc tgactgtgtt 360  
 caaagtatca ggaagaacgc cggggaccat gaaacaaatt gtaccctcca ggtttccctc 420  
 aaattctgaa ttctgacatt tggcttcttc aacgtagaat atatcattcg tctcagtctg 480  
 gctgttattg acttctactt ggtaagataa gcatctgcta taaaaatttt gtggattctt 540  
 ccattgcaca tacaagttac cattttggaa gaagagacgc ttaatatggg ggggatcagg 600  
 tttcacatga gaagttaaag gcactatatt gaaggacggg ctaatttttc ttgcattatc 660  
 cttgaccatt atttggacac tgtgttgttc aaaactggaa tccttcaa at tagtcagagc 720  
 aaaggaacaa ccaatgtgtt gaccttctct atagatgtct tcgcattgaa gaatttttcc 780  
 caggctgctg tgccaatagt agagagtata gttgggtgtca gggcttgtat tccttccagg 840  
 aagccaagta cacttcatgt agctcagggt gtgccaaaca cattgtagct cagtcacagc 900  
 cgactcagga tcaccttcag gtggtggggg gcacttttcc accaaaatgc taggattgtc 960  
 actttcattg gtgctgcact gggacccac ttgcagacaa atcctctcat tcaggggtac 1020  
 ttcttttgaa cgatgagttt caggagcaat tttcttatcc tgtttgttgt caaatgact 1080  
 aaaataccgt aaggtgcaat tcgggctggc tccctcggga gggttccatg tccatagac 1140  
 cgtgcagagg ttttcaacag aaacactcaa attcgtcaca ggtggctgag tttcgggtggg 1200  
 tgcggcgacc ccgcc 1215

<210> 54  
 <211> 620  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> CDS  
 <222> (184)..(618)

<400> 54  
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 aattaatgtc tccaaactgg agaagagaaa aaaaagagga cctgtgataa ttgcctatga 120  
 taattcattt cttgagaaac catattattg agtggaaact tcaaagtatt gaatcttgga 180  
 gga atg gct ttc att cat ttg gat gtc gga ttc ctc tat acc ctg ctt 228  
 Met Ala Phe Ile His Leu Asp Val Gly Phe Leu Tyr Thr Leu Leu  
 1 5 10 15



gtt tgc aca gca ttt ggc tct atg ctt tca aat gct gag ata aaa gtt 276  
Val Cys Thr Ala Phe Gly Ser Met Leu Ser Asn Ala Glu Ile Lys Val  
20 25 30

aat cct cct cag gat ttt gag ata gtg gac cct gga tat tta ggt tat 324  
Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr  
35 40 45

ctc tct ttg caa tgg caa cct cca tta ttt ccg gat aat ttt aag gaa 372  
Leu Ser Leu Gln Trp Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu  
50 55 60

tgc aca ata gaa tat gaa tta aaa tac cga aac att gat agt gaa aac 420  
Cys Thr Ile Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn  
65 70 75

tgg aag acc atc att acc aag aat cta cat tac aaa gat ggg ttt gat 468  
Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp  
80 85 90 95

ctt aac aaa ggt att gaa gca aag ata aac aca ctt ctg cca gca caa 516  
Leu Asn Lys Gly Ile Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln  
100 105 110

tgc aca aat gga tca gaa gtt aga agt tca tgg gca gaa act act tat 564  
Cys Thr Asn Gly Ser Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr  
115 120 125

tgg aca tca cca caa gga aat cgg gaa act aaa att caa gat atg gac 612  
Trp Thr Ser Pro Gln Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp  
130 135 140

tgt gta ta 620  
Cys Val  
145

<210> 55  
<211> 145  
<212> PRT  
<213> Canis familiaris

<400> 55  
Met Ala Phe Ile His Leu Asp Val Gly Phe Leu Tyr Thr Leu Leu Val  
1 5 10 15

Cys Thr Ala Phe Gly Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn

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Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu		
35	40	45
Ser Leu Gln Trp Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys		
50	55	60
Thr Ile Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp		
65	70	75 80
Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu		
85	90	95
Asn Lys Gly Ile Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys		
100	105	110
Thr Asn Gly Ser Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp		
115	120	125
Thr Ser Pro Gln Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys		
130	135	140

Val  
145

<210> 56  
<211> 620  
<212> DNA  
<213> Canis familiaris

<400> 56  
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gtagtttctg cccatgaact tctaacttct gatccatttg tgcattgtgc tggcagaagt 120  
gtgtttatct ttgcttcaat acctttgtta agatcaaacc catctttgta atgtagattc 180  
ttggtaaatga tgggtcttcca gttttcacta tcaatgtttc ggtattttta ttcattattct 240  
attgtgcatt ccttaaaatt atccggaaat aatggagggt gccattgcaa agagagataa 300  
cctaaatatc cagggtccac tatctcaaaa tcctgaggag gattaacttt tatctcagca 360  
tttgaaagca tagagccaaa tgctgtgcaa acaagcaggg tatagaggaa tccgacatcc 420  
aaatgaatga aagccattcc tccaagattc aatactttga agtttccact caataatatg 480  
gtttctcaag aaatgaatta tcataggcaa ttatcacagg tcctcttttt tttctcttct 540  
ccagtttgga gacattaatt agaattctta agacttcctt tcctgtctga taatcaagca 600  
caciaactca gcctcgtgcc 620

<210> 57

<211> 878  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> CDS  
 <222> (1)..(765)

<220>  
 <221> misc\_feature  
 <222> (862)  
 <223> At position 862, n = unknown

<400> 57  
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 Gln Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr  
 1 5 10 15  
 aac tgg caa tat tta gtc tgc tct tgg aaa cct ggc atg ggt gtc cat 96  
 Asn Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His  
 20 25 30  
 ttt gat acc aat tac cag ttg ttt tac tgg tat gag ggc ttg gac cat 144  
 Phe Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His  
 35 40 45  
 tca gca gag tgt act gat tac atc aag gtt aat gga aaa aat atg gga 192  
 Ser Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly  
 50 55 60  
 tgc agg ttt ccc tat ttg gag tca tca gac tat aaa gat ttc tac atc 240  
 Cys Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile  
 65 70 75 80  
 tgt gtt aat ggg tca tca gaa tcc cag cct atc aga ccc agc tat ttt 288  
 Cys Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe  
 85 90 95  
 att ttt cag ctt caa aat ata gtt aaa cct atg cca cca gac tac ctt 336  
 Ile Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu  
 100 105 110  
 agt ctt act gtg aag aat tca gag gaa att aac ctg aaa tgg aac atg 384  
 Ser Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met  
 115 120 125  
 cct aaa gga ccc att cca gcc aaa tgt ttc att tat gaa att gaa ttc 432  
 Pro Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe



35	40	45
Ser Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly		
50	55	60
Cys Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile		
65	70	75
Cys Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe		
85	90	95
Ile Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu		
100	105	110
Ser Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met		
115	120	125
Pro Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe		
130	135	140
Thr Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile		
145	150	155
Gln Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val		
165	170	175
Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu		
180	185	190
Trp Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Leu		
195	200	205
Val Phe Phe Leu Ile Pro Phe Ala Phe Val Ser Ile Phe Val Leu Val		
210	215	220
Ile Thr Cys Leu Leu Leu Tyr Lys Gln Arg Ala Leu Leu Lys Thr Ile		
225	230	235
Phe His Thr Lys Lys Glu Val Phe Ser His Gln Asp Thr Phe Cys		
245	250	255

<210> 59  
 <211> 878  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> misc\_feature  
 <222> (17)  
 <223> At position 17, n = unknown

<400> 59  
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 ttaataagac tcatatttaa catctggcca taagactgaa agttactgag tcaacagaat 120  
 gtgtcttgat gagaaaagac ttcttttttt gtatgaaaga tcgttttcag taaagccctt 180  
 tgcttatata aaagcaggca agttattacc aaaacaaata ttgagacaaa agcaaagtgt 240  
 atcaagaaaa atactaaggt ttcccttccat atgtcacctt tccagcattg ttcactactc 300  
 cactcactcc agattccatc atctgagcaa taaatattca ctttacttct taccaaaaag 360  
 cataattttt ggcttttcatt tgatgttctt gtgatttgta tctcattctc aactgtggta 420  
 gtcacccaag tagtaccatc ctctgtgaat tcaatttcat aaatgaaaca tttggctgga 480  
 atgggtcctt taggcatggt ccatttcagg ttaatttcct ctgaattctt cacagtaaga 540  
 ctaaggtagt ctggtggcat aggtttaact atattttgaa gctgaaaaat aaaatagctg 600  
 ggtctgatag gctgggattc tgatgacca ttaacacaga tgtagaaatc tttatagtct 660  
 gatgactcca aatagggaaa cctgcacccc atattttttc cattaacctt gatgtaatca 720  
 gtacactctg ctgaatgggc caagccctca taccagtaaa acaactggta attggtatca 780  
 aaatggacac ccatgccagg ttccaagag cagactaaat attgccagtt gtaatataca 840  
 cagtccatat cttgaatttt agtttcccga tttccttg 878

<210> 60  
 <211> 1454  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> CDS  
 <222> (184)..(1341)

<220>  
 <221> misc\_feature  
 <222> (1438)  
 <223> At position 1438, n = unknown

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 aattaatgtc tccaaactgg agaagagaaa aaaaagagga cctgtgataa ttgcctatga 120  
 taattcattt cttgagaaac catattattg agtggaaact tcaaagtatt gaatcttgga 180  
 gga atg gct ttc att cat ttg gat gtc gga ttc ctc tat acc ctg ctt 228  
 Met Ala Phe Ile His Leu Asp Val Gly Phe Leu Tyr Thr Leu Leu  
 1 5 10 15

gtt tgc aca gca ttt ggc tct atg ctt tca aat gct gag ata aaa gtt	276
Val Cys Thr Ala Phe Gly Ser Met Leu Ser Asn Ala Glu Ile Lys Val	
20 25 30	
aat cct cct cag gat ttt gag ata gtg gac cct gga tat tta ggt tat	324
Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr	
35 40 45	
ctc tct ttg caa tgg caa cct cca tta ttt ccg gat aat ttt aag gaa	372
Leu Ser Leu Gln Trp Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu	
50 55 60	
tgc aca ata gaa tat gaa tta aaa tac cga aac att gat agt gaa aac	420
Cys Thr Ile Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn	
65 70 75	
tgg aag acc atc att acc aag aat cta cat tac aaa gat ggg ttt gat	468
Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp	
80 85 90 95	
ctt aac aaa ggt att gaa gca aag ata aac aca ctt ctg cca gca caa	516
Leu Asn Lys Gly Ile Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln	
100 105 110	
tgc aca aat gga tca gaa gtt aga agt tca tgg gca gaa act act tat	564
Cys Thr Asn Gly Ser Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr	
115 120 125	
tgg aca tca cca caa gga aat cgg gaa act aaa att caa gat atg gac	612
Trp Thr Ser Pro Gln Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp	
130 135 140	
tgt gta tat tac aac tgg caa tat tta gtc tgc tct tgg aaa cct ggc	660
Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly	
145 150 155	
atg ggt gtc cat ttt gat acc aat tac cag ttg ttt tac tgg tat gag	708
Met Gly Val His Phe Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu	
160 165 170 175	
ggc ttg gac cat tca gca gag tgt act gat tac atc aag gtt aat gga	756
Gly Leu Asp His Ser Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly	
180 185 190	
aaa aat atg gga tgc agg ttt ccc tat ttg gag tca tca gac tat aaa	804
Lys Asn Met Gly Cys Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys	
195 200 205	

gat ttc tac atc tgt gtt aat ggg tca tca gaa tcc cag cct atc aga	852
Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg	
210 215 220	
ccc agc tat ttt att ttt cag ctt caa aat ata gtt aaa cct atg cca	900
Pro Ser Tyr Phe Ile Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro	
225 230 235	
cca gac tac ctt agt ctt act gtg aag aat tca gag gaa att aac ctg	948
Pro Asp Tyr Leu Ser Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu	
240 245 250 255	
aaa tgg aac atg cct aaa gga ccc att cca gcc aaa tgt ttc att tat	996
Lys Trp Asn Met Pro Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr	
260 265 270	
gaa att gaa ttc aca gag gat ggt act act tgg gtg act acc aca gtt	1044
Glu Ile Glu Phe Thr Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val	
275 280 285	
gag aat gag ata caa atc aca aga aca tca aat gaa agc caa aaa tta	1092
Glu Asn Glu Ile Gln Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu	
290 295 300	
tgc ttt ttg gta aga agt aaa gtg aat att tat tgc tca gat gat gga	1140
Cys Phe Leu Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly	
305 310 315	
atc tgg agt gag tgg agt gat gaa caa tgc tgg aaa ggt gac ata tgg	1188
Ile Trp Ser Glu Trp Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp	
320 325 330 335	
aag gaa acc tta gta ttt ttc ttg ata cca ttt gct ttt gtc tca ata	1236
Lys Glu Thr Leu Val Phe Phe Leu Ile Pro Phe Ala Phe Val Ser Ile	
340 345 350	
ttt gtt ttg gta ata act tgc ctg ctt ttg tat aag caa agg gct tta	1284
Phe Val Leu Val Ile Thr Cys Leu Leu Leu Tyr Lys Gln Arg Ala Leu	
355 360 365	
ctg aaa acg atc ttt cat aca aaa aaa gaa gtc ttt tct cat caa gac	1332
Leu Lys Thr Ile Phe His Thr Lys Lys Glu Val Phe Ser His Gln Asp	
370 375 380	
aca ttc tgt tgactcagta actttcagtc ttatggccag atgttaaata	1381
Thr Phe Cys	
385	



tgagtcttat taaactgaag cttttcctca aatattgaat aaatcttatt ttaaaangaa 1441

aaaaaaaaaa aaa

1454

<210> 61

<211> 386

<212> PRT

<213> Canis familiaris

<400> 61

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1

5

10

15

Cys Thr Ala Phe Gly Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn

20

25

30

Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu

35

40

45

Ser Leu Gln Trp Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys

50

55

60

Thr Ile Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp

65

70

75

80

Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu

85

90

95

Asn Lys Gly Ile Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys

100

105

110

Thr Asn Gly Ser Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp

115

120

125

Thr Ser Pro Gln Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys

130

135

140

Val Tyr Tyr Asn Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met

145

150

155

160

Gly Val His Phe Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly

165

170

175

Leu Asp His Ser Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys

180

185

190

Asn Met Gly Cys Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp

195	200	205
Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro		
210	215	220
Ser Tyr Phe Ile Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro		
225	230	235 240
Asp Tyr Leu Ser Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys		
	245	250 255
Trp Asn Met Pro Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu		
	260	265 270
Ile Glu Phe Thr Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu		
	275	280 285
Asn Glu Ile Gln Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys		
	290	295 300
Phe Leu Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile		
305	310	315 320
Trp Ser Glu Trp Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys		
	325	330 335
Glu Thr Leu Val Phe Phe Leu Ile Pro Phe Ala Phe Val Ser Ile Phe		
	340	345 350
Val Leu Val Ile Thr Cys Leu Leu Leu Tyr Lys Gln Arg Ala Leu Leu		
	355	360 365
Lys Thr Ile Phe His Thr Lys Lys Glu Val Phe Ser His Gln Asp Thr		
	370	375 380
Phe Cys		
385		

<210> 62  
 <211> 1454  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> misc\_feature  
 <222> (17)

<223> At position 17, n = unknown

<400> 62

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gtgtcttgat gagaaaagac ttcttttttt gtatgaaaga tcgttttcag taaagccctt 180
tgcttatata aaagcaggca agttattacc aaaacaaata ttgagacaaa agcaaattggt 240
atcaagaaaa atactaagggt ttccttccat atgtcacctt tccagcattg ttcactcctc 300
cactcactcc agattccatc atctgagcaa taaatattca ctttacttct taccaaaaag 360
cataatnttt ggctttcatt tgatgttctt gtgatttgta tctcattctc aactgtggta 420
gtcacccaag tagtaccatc ctctgtgaat tcaatttcat aaatgaaaca tttggctgga 480
atgggtcctt taggcattgt ccatttcagg ttaatttctt ctgaattctt cacagtaaga 540
ctaaggtagt ctgggtggcat aggtttaact atattttgaa gctgaaaaat aaaatagctg 600
gggtctgatag gctgggattc tgatgacca ttaacacaga tgtagaaatc tttatagtct 660
gatgactcca aatagggaaa cctgcattcc atattttttc cattaacctt gatgtaatca 720
gtacactctg ctgaatgggc caagccctca taccagtaaa acaactggta attggtatca 780
aaatggacac ccatgccagg tttccaagag cagactaaat attgccagtt gtaatataca 840
cagtcacatat cttgaatntt agtttcccga tttccttggt gtgatgtcca ataagtagtt 900
tctgcccatt aacttctaac ttctgatcca tttgtgcatt gtgctggcag aagtgtgttt 960
atctttgctt caataccttt gttatgatca aacctatctt tgtaattgat attcttggtt 1020
atgatggtct tccagttttc actatcaatg tttcgggtatt ttaattcata ttctattgtg 1080
cattccttaa aattatccgg aaataatgga ggttgccatt gcaaagagag ataacctaaa 1140
tatccagggt ccactatctc aaaatcctga ggaggattaa cttttatctc agcatttgaa 1200
agcatagagc caaatgctgt gcaaacaagc agggatataga ggaatccgac atccaaatga 1260
atgaaagcca ttctccaag attcaatact ttgaagtttc cactcaataa tatggtttct 1320
caagaaatga attatcatag gcaattatca caggtcctct tttttttctc ttctccagtt 1380
tgagacatt aattagaatc tctaagactt cccttctgt ctgataatca agcacacaaa 1440
ctcagcctcg tgcc 1454
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<210> 63

<211> 1158

<212> DNA

<213> *Canis familiaris*

<400> 63

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gacctggat atttaggtta tctctctttg caatggcaac ctccattatt tccggataat 180
tttaaggaat gcacaataga atatgaatta aaataccgaa acattgatag tgaaaactgg 240
aagaccatca ttaccaagaa tctacattac aaagatgggt ttgatcttaa caaaggattt 300
gaagcaaaga taaacacact tctgccagca caatgcacaa atggatcaga agttagaagt 360
tcatgggcag aaactactta ttggacatca ccacaaggaa atcgggaaac taaaattcaa 420
gatatggact gtgtatatta caactggcaa tatttagtct gctcttgga acctggcatg 480
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gcagagtgtg ctgattacat caaggttaat ggaaaaata tgggatgcag gtttccctat 600
ttggagtcac cagactataa agattttctac atctgtgtta atgggtcatc agaatccag 660
cctatcagac ccagctatntt tatttttcag cttcaaaata tagttaaacc tatgccacca 720
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gactacctta gtcttactgt gaagaattca gaggaaatta acctgaaatg gaacatgcct 780
aaaggaccca ttccagccaa atgttttcatt tatgaaattg aattcacaga ggatgggtact 840
acttgggtga ctaccacagt tgagaatgag atacaaatca caagaacatc aaatgaaagc 900
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<210> 64

<211> 1158

<212> DNA

<213> *Canis familiaris*

<400> 64

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aaatgggtatc aagaaaaata ctaagggtttc cttccatattg tcacctttcc agcattgttc 180
atcactccac tcaactccaga ttccatcatc tgagcaataa atattcactt tacttcttac 240
caaaaagcat aattttttggc tttcatttga tgttcttgtg atttgtatct cattctcaac 300
tgtggtagtc acccaagtag taccatcctc tgtgaattca atttcataaa tgaaacattt 360
ggctggaatg ggtccttttag gcatgttcca tttcagggtta atttcctctg aattcttcac 420
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atagctgggt ctgataggct gggattctga tgaccatta acacagatgt agaaatcttt 540
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gtaatcagta cactctgctg aatgggtcca gccctcatc cagtaaaaca actggtaatt 660
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atgtgaaagc atagagccaa atgctgtgca aacaagcagg gtatagagga atccgacatc 1140
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<210> 65

<211> 1095

<212> DNA

<213> *Canis familiaris*

<220>

<221> CDS

<222> (1) .. (1095)

<400> 65

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1 5 10 15	
 gag ata gtg gac cct gga tat tta ggt tat ctc tct ttg caa tgg caa	96
Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp Gln	
20 25 30	
 cct cca tta ttt ccg gat aat ttt aag gaa tgc aca ata gaa tat gaa	144
Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr Glu	
35 40 45	
 tta aaa tac cga aac att gat agt gaa aac tgg aag acc atc att acc	192
Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile Thr	
50 55 60	
 aag aat cta cat tac aaa gat ggg ttt gat ctt aac aaa ggt att gaa	240
Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile Glu	
65 70 75 80	
 gca aag ata aac aca ctt ctg cca gca caa tgc aca aat gga tca gaa	288
Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser Glu	
85 90 95	
 gtt aga agt tca tgg gca gaa act act tat tgg aca tca cca caa gga	336
Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln Gly	
100 105 110	
 aat cgg gaa act aaa att caa gat atg gac tgt gta tat tac aac tgg	384
Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn Trp	
115 120 125	
 caa tat tta gtc tgc tct tgg aaa cct ggc atg ggt gtc cat ttt gat	432
Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe Asp	
130 135 140	
 acc aat tac cag ttg ttt tac tgg tat gag ggc ttg gac cat tca gca	480
Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser Ala	
145 150 155 160	
 gag tgt act gat tac atc aag gtt aat gga aaa aat atg gga tgc agg	528
Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys Arg	
165 170 175	
 ttt ccc tat ttg gag tca tca gac tat aaa gat ttc tac atc tgt gtt	576
Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys Val	
180 185 190	

aat ggg tca tca gaa tcc cag cct atc aga ccc agc tat ttt att ttt	624
Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile Phe	
195 200 205	
cag ctt caa aat ata gtt aaa cct atg cca cca gac tac ctt agt ctt	672
Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser Leu	
210 215 220	
act gtg aag aat tca gag gaa att aac ctg aaa tgg aac atg cct aaa	720
Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro Lys	
225 230 235 240	
gga ccc att cca gcc aaa tgt ttc att tat gaa att gaa ttc aca gag	768
Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr Glu	
245 250 255	
gat ggt act act tgg gtg act acc aca gtt gag aat gag ata caa atc	816
Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln Ile	
260 265 270	
aca aga aca tca aat gaa agc caa aaa tta tgc ttt ttg gta aga agt	864
Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg Ser	
275 280 285	
aaa gtg aat att tat tgc tca gat gat gga atc tgg agt gag tgg agt	912
Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp Ser	
290 295 300	
gat gaa caa tgc tgg aaa ggt gac ata tgg aag gaa acc tta gta ttt	960
Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Leu Val Phe	
305 310 315 320	
ttc ttg ata cca ttt gct ttt gtc tca ata ttt gtt ttg gta ata act	1008
Phe Leu Ile Pro Phe Ala Phe Val Ser Ile Phe Val Leu Val Ile Thr	
325 330 335	
tgc ctg ctt ttg tat aag caa agg gct tta ctg aaa acg atc ttt cat	1056
Cys Leu Leu Leu Tyr Lys Gln Arg Ala Leu Leu Lys Thr Ile Phe His	
340 345 350	
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Thr Lys Lys Glu Val Phe Ser His Gln Asp Thr Phe Cys	
355 360 365	

<210> 66  
 <211> 365  
 <212> PRT

<213> Canis familiaris

<400> 66

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Glu	Ile	Val	Asp	Pro	Gly	Tyr	Leu	Gly	Tyr	Leu	Ser	Leu	Gln	Trp	Gln
			20					25					30		
Pro	Pro	Leu	Phe	Pro	Asp	Asn	Phe	Lys	Glu	Cys	Thr	Ile	Glu	Tyr	Glu
		35					40					45			
Leu	Lys	Tyr	Arg	Asn	Ile	Asp	Ser	Glu	Asn	Trp	Lys	Thr	Ile	Ile	Thr
	50					55					60				
Lys	Asn	Leu	His	Tyr	Lys	Asp	Gly	Phe	Asp	Leu	Asn	Lys	Gly	Ile	Glu
65					70					75				80	
Ala	Lys	Ile	Asn	Thr	Leu	Leu	Pro	Ala	Gln	Cys	Thr	Asn	Gly	Ser	Glu
				85					90					95	
Val	Arg	Ser	Ser	Trp	Ala	Glu	Thr	Thr	Tyr	Trp	Thr	Ser	Pro	Gln	Gly
			100					105					110		
Asn	Arg	Glu	Thr	Lys	Ile	Gln	Asp	Met	Asp	Cys	Val	Tyr	Tyr	Asn	Trp
		115					120					125			
Gln	Tyr	Leu	Val	Cys	Ser	Trp	Lys	Pro	Gly	Met	Gly	Val	His	Phe	Asp
	130					135					140				
Thr	Asn	Tyr	Gln	Leu	Phe	Tyr	Trp	Tyr	Glu	Gly	Leu	Asp	His	Ser	Ala
145					150					155					160
Glu	Cys	Thr	Asp	Tyr	Ile	Lys	Val	Asn	Gly	Lys	Asn	Met	Gly	Cys	Arg
			165						170					175	
Phe	Pro	Tyr	Leu	Glu	Ser	Ser	Asp	Tyr	Lys	Asp	Phe	Tyr	Ile	Cys	Val
			180					185					190		
Asn	Gly	Ser	Ser	Glu	Ser	Gln	Pro	Ile	Arg	Pro	Ser	Tyr	Phe	Ile	Phe
		195					200					205			
Gln	Leu	Gln	Asn	Ile	Val	Lys	Pro	Met	Pro	Pro	Asp	Tyr	Leu	Ser	Leu
	210					215					220				
Thr	Val	Lys	Asn	Ser	Glu	Glu	Ile	Asn	Leu	Lys	Trp	Asn	Met	Pro	Lys
225					230					235					240

Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr Glu  
245 250 255

Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln Ile  
260 265 270

Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg Ser  
275 280 285

Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp Ser  
290 295 300

Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Leu Val Phe  
305 310 315 320

Phe Leu Ile Pro Phe Ala Phe Val Ser Ile Phe Val Leu Val Ile Thr  
325 330 335

Cys Leu Leu Leu Tyr Lys Gln Arg Ala Leu Leu Lys Thr Ile Phe His  
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Thr Lys Lys Glu Val Phe Ser His Gln Asp Thr Phe Cys  
355 360 365

<210> 67

<211> 1095

<212> DNA

<213> Canis familiaris

<400> 67

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aatgggtatc aagaaaaata ctaagggttc cttccatattg tcacctttcc agcattgttc 180  
atcactccac tcaactccaga ttccatcatc tgagcaataa atattcactt tacttcttac 240  
caaaaagcat aatttttggc tttcatttga tgttcttggtg atttgtatct cattctcaac 300  
tgtggtagtc acccaagtag taccatcctc tgtgaattca atttcataaa tgaaacattt 360  
ggctggaatg ggctcctttag gcatgttcca tttcagggtta atttcctctg aattcttcac 420  
agtaagacta aggtagtctg gtggcatagg tttaactata ttttgaagct gaaaaataaa 480  
atagctgggt ctgataggct gggattctga tgaccatta acacagatgt agaaatcttt 540  
atagtctgat gactccaaat agggaaacct gcatcccata ttttttccat taaccttgat 600  
gtaatcagta cactctgctg aatgggtcca gccctcatalc cagtaaaaca actggtaatt 660  
ggatatcaaaa tggacaccca tgccagggtt ccaagagcag actaaatatt gccagttgta 720  
atatacacag tccatatctt gaattttagt ttcccgattt ccttgtgggtg atgtccaata 780  
agtagtttct gcccatgaac ttctaacttc tgatccattt gtgcattgtg ctggcagaag 840  
tgtgtttatc tttgcttcaa tacctttggt aagatcaaac ccatctttgt aatgtagatt 900  
cttggtaatg atgggtcttc agttttcact atcaatgttt cggtatttta attcatattc 960



tattgtgcat tccttaaaat tatccggaaa taatggaggt tgccattgca aagagagata 1020  
 acctaaatat ccaggggtcca ctatctcaaa atcctgagga ggattaactt ttatctcagc 1080  
 atttgaaagc ataga 1095

<210> 68  
 <211> 954  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> CDS  
 <222> (1)..(954)

<400> 68  
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 1 5 10 15  
 ttt gag ata gtg gac cct gga tat tta ggt tat ctc tct ttg caa tgg 96  
 Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp  
 20 25 30  
 caa cct cca tta ttt ccg gat aat ttt aag gaa tgc aca ata gaa tat 144  
 Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr  
 35 40 45  
 gaa tta aaa tac cga aac att gat agt gaa aac tgg aag acc atc att 192  
 Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile  
 50 55 60  
 acc aag aat cta cat tac aaa gat ggg ttt gat ctt aac aaa ggt att 240  
 Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile  
 65 70 75 80  
 gaa gca aag ata aac aca ctt ctg cca gca caa tgc aca aat gga tca 288  
 Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser  
 85 90 95  
 gaa gtt aga agt tca tgg gca gaa act act tat tgg aca tca cca caa 336  
 Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln  
 100 105 110  
 gga aat cgg gaa act aaa att caa gat atg gac tgt gta tat tac aac 384  
 Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn  
 115 120 125  
 tgg caa tat tta gtc tgc tct tgg aaa cct ggc atg ggt gtc cat ttt 432

Trp	Gln	Tyr	Leu	Val	Cys	Ser	Trp	Lys	Pro	Gly	Met	Gly	Val	His	Phe		
130						135					140						
gat	acc	aat	tac	cag	ttg	ttt	tac	tgg	tat	gag	ggc	ttg	gac	cat	tca	480	
Asp	Thr	Asn	Tyr	Gln	Leu	Phe	Tyr	Trp	Tyr	Glu	Gly	Leu	Asp	His	Ser		
145					150					155					160		
gca	gag	tgt	act	gat	tac	atc	aag	gtt	aat	gga	aaa	aat	atg	gga	tgc	528	
Ala	Glu	Cys	Thr	Asp	Tyr	Ile	Lys	Val	Asn	Gly	Lys	Asn	Met	Gly	Cys		
				165					170					175			
agg	ttt	ccc	tat	ttg	gag	tca	tca	gac	tat	aaa	gat	ttc	tac	atc	tgt	576	
Arg	Phe	Pro	Tyr	Leu	Glu	Ser	Ser	Asp	Tyr	Lys	Asp	Phe	Tyr	Ile	Cys		
			180					185					190				
gtt	aat	ggg	tca	tca	gaa	tcc	cag	cct	atc	aga	ccc	agc	tat	ttt	att	624	
Val	Asn	Gly	Ser	Ser	Glu	Ser	Gln	Pro	Ile	Arg	Pro	Ser	Tyr	Phe	Ile		
	195						200					205					
ttt	cag	ctt	caa	aat	ata	gtt	aaa	cct	atg	cca	cca	gac	tac	ctt	agt	672	
Phe	Gln	Leu	Gln	Asn	Ile	Val	Lys	Pro	Met	Pro	Pro	Asp	Tyr	Leu	Ser		
	210				215					220							
ctt	act	gtg	aag	aat	tca	gag	gaa	att	aac	ctg	aaa	tgg	aac	atg	cct	720	
Leu	Thr	Val	Lys	Asn	Ser	Glu	Glu	Ile	Asn	Leu	Lys	Trp	Asn	Met	Pro		
225					230					235					240		
aaa	gga	ccc	att	cca	gcc	aaa	tgt	ttc	att	tat	gaa	att	gaa	ttc	aca	768	
Lys	Gly	Pro	Ile	Pro	Ala	Lys	Cys	Phe	Ile	Tyr	Glu	Ile	Glu	Phe	Thr		
				245					250					255			
gag	gat	ggg	act	act	tgg	gtg	act	acc	aca	gtt	gag	aat	gag	ata	caa	816	
Glu	Asp	Gly	Thr	Thr	Trp	Val	Thr	Thr	Thr	Val	Glu	Asn	Glu	Ile	Gln		
			260					265					270				
atc	aca	aga	aca	tca	aat	gaa	agc	caa	aaa	tta	tgc	ttt	ttg	gta	aga	864	
Ile	Thr	Arg	Thr	Ser	Asn	Glu	Ser	Gln	Lys	Leu	Cys	Phe	Leu	Val	Arg		
			275					280					285				
agt	aaa	gtg	aat	att	tat	tgc	tca	gat	gat	gga	atc	tgg	agt	gag	tgg	912	
Ser	Lys	Val	Asn	Ile	Tyr	Cys	Ser	Asp	Asp	Gly	Ile	Trp	Ser	Glu	Trp		
	290					295				300							
agt	gat	gaa	caa	tgc	tgg	aaa	ggg	gat	atc	tgg	aag	gaa	acc			954	
Ser	Asp	Glu	Gln	Cys	Trp	Lys	Gly	Asp	Ile	Trp	Lys	Glu	Thr				
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<210> 69  
 <211> 318  
 <212> PRT  
 <213> Canis familiaris

<400> 69

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Phe	Glu	Ile	Val	Asp	Pro	Gly	Tyr	Leu	Gly	Tyr	Leu	Ser	Leu	Gln	Trp
			20					25					30		

Gln	Pro	Pro	Leu	Phe	Pro	Asp	Asn	Phe	Lys	Glu	Cys	Thr	Ile	Glu	Tyr
		35					40					45			

Glu	Leu	Lys	Tyr	Arg	Asn	Ile	Asp	Ser	Glu	Asn	Trp	Lys	Thr	Ile	Ile
	50					55					60				

Thr	Lys	Asn	Leu	His	Tyr	Lys	Asp	Gly	Phe	Asp	Leu	Asn	Lys	Gly	Ile
65					70					75					80

Glu	Ala	Lys	Ile	Asn	Thr	Leu	Leu	Pro	Ala	Gln	Cys	Thr	Asn	Gly	Ser
				85					90					95	

Glu	Val	Arg	Ser	Ser	Trp	Ala	Glu	Thr	Thr	Tyr	Trp	Thr	Ser	Pro	Gln
			100					105					110		

Gly	Asn	Arg	Glu	Thr	Lys	Ile	Gln	Asp	Met	Asp	Cys	Val	Tyr	Tyr	Asn
	115						120					125			

Trp	Gln	Tyr	Leu	Val	Cys	Ser	Trp	Lys	Pro	Gly	Met	Gly	Val	His	Phe
	130					135					140				

Asp	Thr	Asn	Tyr	Gln	Leu	Phe	Tyr	Trp	Tyr	Glu	Gly	Leu	Asp	His	Ser
145					150					155				160	

Ala	Glu	Cys	Thr	Asp	Tyr	Ile	Lys	Val	Asn	Gly	Lys	Asn	Met	Gly	Cys
				165					170					175	

Arg	Phe	Pro	Tyr	Leu	Glu	Ser	Ser	Asp	Tyr	Lys	Asp	Phe	Tyr	Ile	Cys
			180					185					190		

Val	Asn	Gly	Ser	Ser	Glu	Ser	Gln	Pro	Ile	Arg	Pro	Ser	Tyr	Phe	Ile
	195						200					205			

Phe	Gln	Leu	Gln	Asn	Ile	Val	Lys	Pro	Met	Pro	Pro	Asp	Tyr	Leu	Ser
	210					215					220				

Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro  
 225 230 235 240

Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr  
 245 250 255

Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln  
 260 265 270

Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg  
 275 280 285

Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp  
 290 295 300

Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr  
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<210> 70

<211> 954

<212> DNA

<213> Canis familiaris

<400> 70

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atttgatgtt cttgtgattt gtatctcatt ctcaactgtg gtagtcaccc aagtagtacc 180
atcctctgtg aattcaattt cataaatgaa acatttggct ggaatgggtc ctttaggcac 240
gttcattttc aggttaattt cctctgaatt cttcacagta agactaaggt agtctggtgg 300
cataggttta actatatttt gaagctgaaa aataaaatag ctgggtctga taggctggga 360
ttctgatgac ccattaacac agatgtagaa atctttatag tctgatgact ccaaataagg 420
aaacctgcat cccatatttt ttccattaac cttgatgtaa tcagtacact ctgctgaatg 480
gtccaagccc tcataaccagt aaaacaactg gtaattggta tcaaaatgga cacccatgcc 540
aggttttcaa gagcagacta aatattgcc a gttgtaatat acacagtcca tatcttgaat 600
tttagtttcc cgatttcctt gtggtgatgt ccaataagta gtttctgccc atgaacttct 660
aacttctgat ccatttgtgc attgtgctgg cagaagtgtg .tttatcttg cttcaatacc 720
tttgtaaga tcaaaccat ctttgtaatg tagattcttg gtaatgatgg tcttccagtt 780
ttcactatca atgtttcggc attttaattc atattctatt gtgcattcct taaaattatc 840
cggaaataat ggaggttgcc attgcaaaga gagataacct aaatatccag ggtccactat 900
ctcaaaatcc tgaggaggat taacttttat ctcagcattt gaaagcatag acat 954

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<210> 71

<211> 1686

<212> DNA

<213> Canis familiaris

<220>

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<222> (1)..(1683)

<400> 71

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Met	Ser	Met	Leu	Ser	Asn	Ala	Glu	Ile	Lys	Val	Asn	Pro	Pro	Gln	Asp	
1				5					10					15		

ttt	gag	ata	gtg	gac	cct	gga	tat	tta	ggg	tat	ctc	tct	ttg	caa	tgg	96
Phe	Glu	Ile	Val	Asp	Pro	Gly	Tyr	Leu	Gly	Tyr	Leu	Ser	Leu	Gln	Trp	
			20					25					30			

caa	cct	cca	tta	ttt	ccg	gat	aat	ttt	aag	gaa	tgc	aca	ata	gaa	tat	144
Gln	Pro	Pro	Leu	Phe	Pro	Asp	Asn	Phe	Lys	Glu	Cys	Thr	Ile	Glu	Tyr	
		35					40					45				

gaa	tta	aaa	tac	cga	aac	att	gat	agt	gaa	aac	tgg	aag	acc	atc	att	192
Glu	Leu	Lys	Tyr	Arg	Asn	Ile	Asp	Ser	Glu	Asn	Trp	Lys	Thr	Ile	Ile	
	50					55					60					

acc	aag	aat	cta	cat	tac	aaa	gat	ggg	ttt	gat	ctt	aac	aaa	ggg	att	240
Thr	Lys	Asn	Leu	His	Tyr	Lys	Asp	Gly	Phe	Asp	Leu	Asn	Lys	Gly	Ile	
	65				70				75					80		

gaa	gca	aag	ata	aac	aca	ctt	ctg	cca	gca	caa	tgc	aca	aat	gga	tca	288
Glu	Ala	Lys	Ile	Asn	Thr	Leu	Leu	Pro	Ala	Gln	Cys	Thr	Asn	Gly	Ser	
				85				90						95		

gaa	gtt	aga	agt	tca	tgg	gca	gaa	act	act	tat	tgg	aca	tca	cca	caa	336
Glu	Val	Arg	Ser	Ser	Trp	Ala	Glu	Thr	Thr	Tyr	Trp	Thr	Ser	Pro	Gln	
			100				105						110			

gga	aat	cgg	gaa	act	aaa	att	caa	gat	atg	gac	tgt	gta	tat	tac	aac	384
Gly	Asn	Arg	Glu	Thr	Lys	Ile	Gln	Asp	Met	Asp	Cys	Val	Tyr	Tyr	Asn	
		115					120					125				

tgg	caa	tat	tta	gtc	tgc	tct	tgg	aaa	cct	ggc	atg	ggg	gtc	cat	ttt	432
Trp	Gln	Tyr	Leu	Val	Cys	Ser	Trp	Lys	Pro	Gly	Met	Gly	Val	His	Phe	
	130					135					140					

gat	acc	aat	tac	cag	ttg	ttt	tac	tgg	tat	gag	ggc	ttg	gac	cat	tca	480
Asp	Thr	Asn	Tyr	Gln	Leu	Phe	Tyr	Trp	Tyr	Glu	Gly	Leu	Asp	His	Ser	
145					150					155				160		

gca	gag	tgt	act	gat	tac	atc	aag	gtt	aat	gga	aaa	aat	atg	gga	tgc	528
Ala	Glu	Cys	Thr	Asp	Tyr	Ile	Lys	Val	Asn	Gly	Lys	Asn	Met	Gly	Cys	

165	170	175	
agg ttt ccc tat ttg gag tca tca gac tat aaa gat ttc tac atc tgt			576
Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys			
180	185	190	
gtt aat ggg tca tca gaa tcc cag cct atc aga ccc agc tat ttt att			624
Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile			
195	200	205	
ttt cag ctt caa aat ata gtt aaa cct atg cca cca gac tac ctt agt			672
Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser			
210	215	220	
ctt act gtg aag aat tca gag gaa att aac ctg aaa tgg aac atg cct			720
Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro			
225	230	235	240
aaa gga ccc att cca gcc aaa tgt ttc att tat gaa att gaa ttc aca			768
Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr			
245	250	255	
gag gat ggt act act tgg gtg act acc aca gtt gag aat gag ata caa			816
Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln			
260	265	270	
atc aca aga aca tca aat gaa agc caa aaa tta tgc ttt ttg gta aga			864
Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg			
275	280	285	
agt aaa gtg aat att tat tgc tca gat gat gga atc tgg agt gag tgg			912
Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp			
290	295	300	
agt gat gaa caa tgc tgg aaa ggt gat atc tgg aag gaa acc gga tcc			960
Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Gly Ser			
305	310	315	320
aac act aaa gta gac aag cca gtg ttc aat gaa tgc aga tgc act gat			1008
Asn Thr Lys Val Asp Lys Pro Val Phe Asn Glu Cys Arg Cys Thr Asp			
325	330	335	
aca ccc cca tgc cca gtc cct gaa cct ctg gga ggg cct tgc gtc ctc			1056
Thr Pro Pro Cys Pro Val Pro Glu Pro Leu Gly Gly Pro Ser Val Leu			
340	345	350	
atc ttt ccc ccg aaa ccc aag gac atc ctc agg att acc cga aca ccc			1104
Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg Ile Thr Arg Thr Pro			

355	360	365	
gag gtc acc tgt gtg gtg tta gat ctg ggc cgt	gag gac cct gag gtg	1152	
Glu Val Thr Cys Val Val Leu Asp Leu Gly Arg	Glu Asp Pro Glu Val		
370	375 380		
cag atc agc tgg ttc gtg gat ggt aag gag gtg	cac aca gcc aag acc	1200	
Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val	His Thr Ala Lys Thr		
385	390 395 400		
cag tct cgt gag cag cag ttc aac ggc acc tac	cgt gtg gtc agc gtc	1248	
Gln Ser Arg Glu Gln Gln Phe Asn Gly Thr Tyr	Arg Val Val Ser Val		
	405 410 415		
ctc ccc att gag cac cag gac tgg ctc aca ggg aag	gag ttc aag tgc	1296	
Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly Lys	Glu Phe Lys Cys		
	420 425 430		
aga gtc aac cac ata gac ctc ccg tct ccc atc	gag agg acc atc tct	1344	
Arg Val Asn His Ile Asp Leu Pro Ser Pro Ile	Glu Arg Thr Ile Ser		
	435 440 445		
aag gcc aga ggg agg gcc cat aag ccc agt gtg	tat gtc ctg ccg cca	1392	
Lys Ala Arg Gly Arg Ala His Lys Pro Ser Val	Tyr Val Leu Pro Pro		
	450 455 460		
tcc cca aag gag ttg tca tcc agt gac aca gtc	agc atc acc tgc ctg	1440	
Ser Pro Lys Glu Leu Ser Ser Ser Asp Thr Val	Ser Ile Thr Cys Leu		
	465 470 475 480		
ata aaa gac ttc tac cca cct gac att gat gtg	gag tgg cag agc aat	1488	
Ile Lys Asp Phe Tyr Pro Pro Asp Ile Asp Val	Glu Trp Gln Ser Asn		
	485 490 495		
gga cag cag gag ccc gag agg aag cac cgc atg	acc ccg ccc cag ctg	1536	
Gly Gln Gln Glu Pro Glu Arg Lys His Arg Met	Thr Pro Pro Gln Leu		
	500 505 510		
gac gag gac ggg tcc tac ttc ctg tac agc aag	ctc tct gtg gac aag	1584	
Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys	Leu Ser Val Asp Lys		
	515 520 525		
agc cgc tgg cag cag gga gac ccc ttc aca tgt	gcg gtg atg cat gaa	1632	
Ser Arg Trp Gln Gln Gly Asp Pro Phe Thr Cys	Ala Val Met His Glu		
	530 535 540		
act cta cag aac cac tac aca gat cta tcc ctc	tcc cat tct ccg ggt	1680	
Thr Leu Gln Asn His Tyr Thr Asp Leu Ser Leu	Ser His Ser Pro Gly		

545

550

555

560

aaa tga

1686

Lys

&lt;210&gt; 72

&lt;211&gt; 561

&lt;212&gt; PRT

&lt;213&gt; Canis familiaris

&lt;400&gt; 72

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Phe	Glu	Ile	Val	Asp	Pro	Gly	Tyr	Leu	Gly	Tyr	Leu	Ser	Leu	Gln	Trp
			20					25					30		

Gln	Pro	Pro	Leu	Phe	Pro	Asp	Asn	Phe	Lys	Glu	Cys	Thr	Ile	Glu	Tyr
	35						40					45			

Glu	Leu	Lys	Tyr	Arg	Asn	Ile	Asp	Ser	Glu	Asn	Trp	Lys	Thr	Ile	Ile
	50					55					60				

Thr	Lys	Asn	Leu	His	Tyr	Lys	Asp	Gly	Phe	Asp	Leu	Asn	Lys	Gly	Ile
65					70					75					80

Glu	Ala	Lys	Ile	Asn	Thr	Leu	Leu	Pro	Ala	Gln	Cys	Thr	Asn	Gly	Ser
				85					90					95	

Glu	Val	Arg	Ser	Ser	Trp	Ala	Glu	Thr	Thr	Tyr	Trp	Thr	Ser	Pro	Gln
			100					105					110		

Gly	Asn	Arg	Glu	Thr	Lys	Ile	Gln	Asp	Met	Asp	Cys	Val	Tyr	Tyr	Asn
	115						120					125			

Trp	Gln	Tyr	Leu	Val	Cys	Ser	Trp	Lys	Pro	Gly	Met	Gly	Val	His	Phe
130						135					140				

Asp	Thr	Asn	Tyr	Gln	Leu	Phe	Tyr	Trp	Tyr	Glu	Gly	Leu	Asp	His	Ser
145					150					155				160	

Ala	Glu	Cys	Thr	Asp	Tyr	Ile	Lys	Val	Asn	Gly	Lys	Asn	Met	Gly	Cys
				165					170					175	

Arg	Phe	Pro	Tyr	Leu	Glu	Ser	Ser	Asp	Tyr	Lys	Asp	Phe	Tyr	Ile	Cys
			180					185					190		



Val	Asn	Gly	Ser	Ser	Glu	Ser	Gln	Pro	Ile	Arg	Pro	Ser	Tyr	Phe	Ile	195	200	205	
Phe	Gln	Leu	Gln	Asn	Ile	Val	Lys	Pro	Met	Pro	Pro	Asp	Tyr	Leu	Ser	210	215	220	
Leu	Thr	Val	Lys	Asn	Ser	Glu	Glu	Ile	Asn	Leu	Lys	Trp	Asn	Met	Pro	225	230	235	240
Lys	Gly	Pro	Ile	Pro	Ala	Lys	Cys	Phe	Ile	Tyr	Glu	Ile	Glu	Phe	Thr	245	250	255	
Glu	Asp	Gly	Thr	Thr	Trp	Val	Thr	Thr	Thr	Val	Glu	Asn	Glu	Ile	Gln	260	265	270	
Ile	Thr	Arg	Thr	Ser	Asn	Glu	Ser	Gln	Lys	Leu	Cys	Phe	Leu	Val	Arg	275	280	285	
Ser	Lys	Val	Asn	Ile	Tyr	Cys	Ser	Asp	Asp	Gly	Ile	Trp	Ser	Glu	Trp	290	295	300	
Ser	Asp	Glu	Gln	Cys	Trp	Lys	Gly	Asp	Ile	Trp	Lys	Glu	Thr	Gly	Ser	305	310	315	320
Asn	Thr	Lys	Val	Asp	Lys	Pro	Val	Phe	Asn	Glu	Cys	Arg	Cys	Thr	Asp	325	330	335	
Thr	Pro	Pro	Cys	Pro	Val	Pro	Glu	Pro	Leu	Gly	Gly	Pro	Ser	Val	Leu	340	345	350	
Ile	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Ile	Leu	Arg	Ile	Thr	Arg	Thr	Pro	355	360	365	
Glu	Val	Thr	Cys	Val	Val	Leu	Asp	Leu	Gly	Arg	Glu	Asp	Pro	Glu	Val	370	375	380	
Gln	Ile	Ser	Trp	Phe	Val	Asp	Gly	Lys	Glu	Val	His	Thr	Ala	Lys	Thr	385	390	395	400
Gln	Ser	Arg	Glu	Gln	Gln	Phe	Asn	Gly	Thr	Tyr	Arg	Val	Val	Ser	Val	405	410	415	
Leu	Pro	Ile	Glu	His	Gln	Asp	Trp	Leu	Thr	Gly	Lys	Glu	Phe	Lys	Cys	420	425	430	
Arg	Val	Asn	His	Ile	Asp	Leu	Pro	Ser	Pro	Ile	Glu	Arg	Thr	Ile	Ser	435	440	445	

Lys Ala Arg Gly Arg Ala His Lys Pro Ser Val Tyr Val Leu Pro Pro  
 450 455 460

Ser Pro Lys Glu Leu Ser Ser Ser Asp Thr Val Ser Ile Thr Cys Leu  
 465 470 475 480

Ile Lys Asp Phe Tyr Pro Pro Asp Ile Asp Val Glu Trp Gln Ser Asn  
 485 490 495

Gly Gln Gln Glu Pro Glu Arg Lys His Arg Met Thr Pro Pro Gln Leu  
 500 505 510

Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys  
 515 520 525

Ser Arg Trp Gln Gln Gly Asp Pro Phe Thr Cys Ala Val Met His Glu  
 530 535 540

Thr Leu Gln Asn His Tyr Thr Asp Leu Ser Leu Ser His Ser Pro Gly  
 545 550 555 560

Lys

<210> 73

<211> 1686

<212> DNA

<213> Canis familiaris

<400> 73

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 gctgtacagg aagtaggacc cgtcctcgtc cagctggggc ggggtcatgc ggtgcttcct 180  
 ctggggctcc tgctgtccat tgctctgcca ctccacatca atgtcagggtg ggtagaagtc 240  
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 ctggtgctca atggggagga cgtgaccac acggtagggtg ccggtgaact gctgctcacg 480  
 agactgggtc ttggctgtgt gcacctcctt accatccacg aaccagctga tctgcacctc 540  
 agggctcctca cggccagat ctaacaccac acaggtgacc tcgggtgttc gggtaatcct 600  
 gaggatgtcc ttgggtttcg ggggaaagat gaggaccgaa ggccctccca gaggttcagg 660  
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 actccagatt ccatcatctg agcaataaat attcacttta cttcttacca aaaagcataa 840  
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tccttttaggc atgtttccatt tcagggttaat ttctctctgaa ttctttcacag taagactaag 1020  
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<210> 74

<211> 1698

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (1)..(1695)

<400> 74

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ttt gag ata gtg gac cct gga tat tta ggt tat ctc tct ttg caa tgg 96  
 Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp  
 20 25 30

caa cct cca tta ttt ccg gat aat ttt aag gaa tgc aca ata gaa tat 144  
 Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr  
 35 40 45

gaa tta aaa tac cga aac att gat agt gaa aac tgg aag acc atc att 192  
 Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile  
 50 55 60

acc aag aat cta cat tac aaa gat ggg ttt gat ctt aac aaa ggt att 240  
 Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile  
 65 70 75 80

gaa gca aag ata aac aca ctt ctg cca gca caa tgc aca aat gga tca 288  
 Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser  
 85 90 95

gaa gtt aga agt tca tgg gca gaa act act tat tgg aca tca cca caa	336
Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln	
100 105 110	
gga aat cgg gaa act aaa att caa gat atg gac tgt gta tat tac aac	384
Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn	
115 120 125	
tgg caa tat tta gtc tgc tct tgg aaa cct ggc atg ggt gtc cat ttt	432
Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe	
130 135 140	
gat acc aat tac cag ttg ttt tac tgg tat gag ggc ttg gac cat tca	480
Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser	
145 150 155 160	
gca gag tgt act gat tac atc aag gtt aat gga aaa aat atg gga tgc	528
Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys	
165 170 175	
agg ttt ccc tat ttg gag tca tca gac tat aaa gat ttc tac atc tgt	576
Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys	
180 185 190	
gtt aat ggg tca tca gaa tcc cag cct atc aga ccc agc tat ttt att	624
Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile	
195 200 205	
ttt cag ctt caa aat ata gtt aaa cct atg cca cca gac tac ctt agt	672
Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser	
210 215 220	
ctt act gtg aag aat tca gag gaa att aac ctg aaa tgg aac atg cct	720
Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro	
225 230 235 240	
aaa gga ccc att cca gcc aaa tgt ttc att tat gaa att gaa ttc aca	768
Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr	
245 250 255	
gag gat ggt act act tgg gtg act acc aca gtt gag aat gag ata caa	816
Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln	
260 265 270	
atc aca aga aca tca aat gaa agc caa aaa tta tgc ttt ttg gta aga	864
Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg	
275 280 285	

agt aaa gtg aat att tat tgc tca gat gat gga atc tgg agt gag tgg	912
Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp	
290 295 300	
agt gat gaa caa tgc tgg aaa ggt gat atc tgg aag gaa acc gga tcc	960
Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Gly Ser	
305 310 315 320	
aac act aaa gta gac aag cca gtg ccc aaa aga gaa aat gga aga gtt	1008
Asn Thr Lys Val Asp Lys Pro Val Pro Lys Arg Glu Asn Gly Arg Val	
325 330 335	
cct cgc cca cct gat tgt ccc aaa tgc cca gcc cct gaa atg ctg gga	1056
Pro Arg Pro Pro Asp Cys Pro Lys Cys Pro Ala Pro Glu Met Leu Gly	
340 345 350	
ggg cct tcg gtc ttc atc ttt ccc ccg aaa ccc aag gac acc ctc ttg	1104
Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Thr Leu Leu	
355 360 365	
att gcc cga aca cct gag gtc aca tgt gtg gtg gtg gat ctg gac cca	1152
Ile Ala Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Leu Asp Pro	
370 375 380	
gaa gac cct gag gtg cag atc agc tgg ttc gtg gac ggt aag cag atg	1200
Glu Asp Pro Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Gln Met	
385 390 395 400	
caa aca gcc aag act cag cct cgt gag gag cag ttc aat ggc acc tac	1248
Gln Thr Ala Lys Thr Gln Pro Arg Glu Glu Gln Phe Asn Gly Thr Tyr	
405 410 415	
cgt gtg gtc agt gtc ctc ccc att ggg cac cag gac tgg ctc aag ggg	1296
Arg Val Val Ser Val Leu Pro Ile Gly His Gln Asp Trp Leu Lys Gly	
420 425 430	
aag cag ttc acg tgc aaa gtc aac aac aaa gcc ctc cca tcc ccg atc	1344
Lys Gln Phe Thr Cys Lys Val Asn Asn Lys Ala Leu Pro Ser Pro Ile	
435 440 445	
gag agg acc atc tcc aag gcc aga ggg caa gcc cat cag ccc agt gtg	1392
Glu Arg Thr Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val	
450 455 460	
tat gtc ctg ccg cca tcc cgg gag gag ttg agc aag aac aca gtc agc	1440
Tyr Val Leu Pro Pro Ser Arg Glu Glu Leu Ser Lys Asn Thr Val Ser	
465 470 475 480	

ttg	aca	tgc	ctg	atc	aaa	gac	ttc	ttc	cca	cct	gac	att	gat	gtg	gag	1488
Leu	Thr	Cys	Leu	Ile	Lys	Asp	Phe	Phe	Pro	Pro	Asp	Ile	Asp	Val	Glu	
				485					490						495	

tgg	cag	agc	aat	gga	cag	cag	gag	cct	gag	agc	aag	tac	cgc	acg	acc	1536
Trp	Gln	Ser	Asn	Gly	Gln	Gln	Glu	Pro	Glu	Ser	Lys	Tyr	Arg	Thr	Thr	
			500					505						510		

ccg	ccc	cag	ctg	gac	gag	gac	ggg	tcc	tac	ttc	ctg	tac	agc	aag	ctc	1584
Pro	Pro	Gln	Leu	Asp	Glu	Asp	Gly	Ser	Tyr	Phe	Leu	Tyr	Ser	Lys	Leu	
		515					520					525				

tct	gtg	gac	aag	agc	cgc	tgg	cag	cgg	gga	gac	acc	ttc	ata	tgt	gcg	1632
Ser	Val	Asp	Lys	Ser	Arg	Trp	Gln	Arg	Gly	Asp	Thr	Phe	Ile	Cys	Ala	
	530					535					540					

gtg	atg	cat	gaa	gct	cta	cac	aac	cac	tac	aca	cag	gaa	tcc	ctc	tcc	1680
Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Glu	Ser	Leu	Ser	
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cat	tct	ccg	ggt	aaa	tga											1698
His	Ser	Pro	Gly	Lys												
				565												

<210> 75  
 <211> 565  
 <212> PRT  
 <213> Canis familiaris

<400> 75															
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Phe	Glu	Ile	Val	Asp	Pro	Gly	Tyr	Leu	Gly	Tyr	Leu	Ser	Leu	Gln	Trp
			20					25					30		
Gln	Pro	Pro	Leu	Phe	Pro	Asp	Asn	Phe	Lys	Glu	Cys	Thr	Ile	Glu	Tyr
			35				40						45		
Glu	Leu	Lys	Tyr	Arg	Asn	Ile	Asp	Ser	Glu	Asn	Trp	Lys	Thr	Ile	Ile
	50					55					60				
Thr	Lys	Asn	Leu	His	Tyr	Lys	Asp	Gly	Phe	Asp	Leu	Asn	Lys	Gly	Ile
65					70					75				80	
Glu	Ala	Lys	Ile	Asn	Thr	Leu	Leu	Pro	Ala	Gln	Cys	Thr	Asn	Gly	Ser

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Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln					
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Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn					
	115		120		125
Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe					
	130		135		140
Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser					
	145		150		155
Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys					
	165		170		175
Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys					
	180		185		190
Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile					
	195		200		205
Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser					
	210		215		220
Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro					
	225		230		235
Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr					
	245		250		255
Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln					
	260		265		270
Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg					
	275		280		285
Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp					
	290		295		300
Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Gly Ser					
	305		310		315
Asn Thr Lys Val Asp Lys Pro Val Pro Lys Arg Glu Asn Gly Arg Val					
	325		330		335
Pro Arg Pro Pro Asp Cys Pro Lys Cys Pro Ala Pro Glu Met Leu Gly					

340	345	350
Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Thr Leu Leu		
355	360	365
Ile Ala Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Leu Asp Pro		
370	375	380
Glu Asp Pro Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Gln Met		
385	390	395
Gln Thr Ala Lys Thr Gln Pro Arg Glu Glu Gln Phe Asn Gly Thr Tyr		
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Arg Val Val Ser Val Leu Pro Ile Gly His Gln Asp Trp Leu Lys Gly		
420	425	430
Lys Gln Phe Thr Cys Lys Val Asn Asn Lys Ala Leu Pro Ser Pro Ile		
435	440	445
Glu Arg Thr Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val		
450	455	460
Tyr Val Leu Pro Pro Ser Arg Glu Glu Leu Ser Lys Asn Thr Val Ser		
465	470	475
Leu Thr Cys Leu Ile Lys Asp Phe Phe Pro Pro Asp Ile Asp Val Glu		
485	490	495
Trp Gln Ser Asn Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg Thr Thr		
500	505	510
Pro Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu		
515	520	525
Ser Val Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile Cys Ala		
530	535	540
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser		
545	550	555
His Ser Pro Gly Lys		
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<210> 76  
 <211> 1698



<212> DNA

<213> *Canis familiaris*

<400> 76

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gctgtacagg aagtaggacc cgtcctcgtc cagctggggc ggggtcgtgc ggtacttgct 180
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at ttgaaagc atagacat 1698
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<210> 77

<211> 1692

<212> DNA

<213> *Canis familiaris*

<220>

<221> CDS

<222> (1)..(1689)

<400> 77

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Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp	
20 25 30	
caa cct cca tta ttt ccg gat aat ttt aag gaa tgc aca ata gaa tat	144
Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr	
35 40 45	
gaa tta aaa tac cga aac att gat agt gaa aac tgg aag acc atc att	192
Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile	
50 55 60	
acc aag aat cta cat tac aaa gat ggg ttt gat ctt aac aaa ggt att	240
Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile	
65 70 75 80	
gaa gca aag ata aac aca ctt ctg cca gca caa tgc aca aat gga tca	288
Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser	
85 90 95	
gaa gtt aga agt tca tgg gca gaa act act tat tgg aca tca cca caa	336
Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln	
100 105 110	
gga aat cgg gaa act aaa att caa gat atg gac tgt gta tat tac aac	384
Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn	
115 120 125	
tgg caa tat tta gtc tgc tct tgg aaa cct ggc atg ggt gtc cat ttt	432
Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe	
130 135 140	
gat acc aat tac cag ttg ttt tac tgg tat gag ggc ttg gac cat tca	480
Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser	
145 150 155 160	
gca gag tgt act gat tac atc aag gtt aat gga aaa aat atg gga tgc	528
Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys	
165 170 175	
agg ttt ccc tat ttg gag tca tca gac tat aaa gat ttc tac atc tgt	576
Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys	
180 185 190	
gtt aat ggg tca tca gaa tcc cag cct atc aga ccc agc tat ttt att	624
Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile	
195 200 205	

ttt cag ctt caa aat ata gtt aaa cct atg cca cca gac tac ctt agt	672
Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser	
210 215 220	
ctt act gtg aag aat tca gag gaa att aac ctg aaa tgg aac atg cct	720
Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro	
225 230 235 240	
aaa gga ccc att cca gcc aaa tgt ttc att tat gaa att gaa ttc aca	768
Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr	
245 250 255	
gag gat ggt act act tgg gtg act acc aca gtt gag aat gag ata caa	816
Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln	
260 265 270	
atc aca aga aca tca aat gaa agc caa aaa tta tgc ttt ttg gta aga	864
Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg	
275 280 285	
agt aaa gtg aat att tat tgc tca gat gat gga atc tgg agt gag tgg	912
Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp	
290 295 300	
agt gat gaa caa tgc tgg aaa ggt gat atc tgg aag gaa acc gga tcc	960
Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Gly Ser	
305 310 315 320	
aac act aaa gta gac aag cca gtg gcc aaa gaa tgc gag tgc aag tgt	1008
Asn Thr Lys Val Asp Lys Pro Val Ala Lys Glu Cys Glu Cys Lys Cys	
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aac tgt aac aac tgc cca tgc cca ggt tgt ggc ctg ctg gga ggg cct	1056
Asn Cys Asn Asn Cys Pro Cys Pro Gly Cys Gly Leu Leu Gly Gly Pro	
340 345 350	
tcg gtc ttc atc ttt ccc cca aaa ccc aag gac atc ctc gtg act gcc	1104
Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Val Thr Ala	
355 360 365	
cgg aca ccc aca gtc act tgt gtg gtg gtg gat ctg gac cca gaa aac	1152
Arg Thr Pro Thr Val Thr Cys Val Val Val Asp Leu Asp Pro Glu Asn	
370 375 380	
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Pro Glu Val Gln Ile Ser Trp Phe Val Asp Ser Lys Gln Val Gln Thr	
385 390 395 400	

gcc aac acg cag cct cgt gag gag cag tcc aat ggc acc tac cgt gtg	1248
Ala Asn Thr Gln Pro Arg Glu Glu Gln Ser Asn Gly Thr Tyr Arg Val	
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gtc agt gtc ctc ccc att ggg cac cag gac tgg ctt tca ggg aag cag	1296
Val Ser Val Leu Pro Ile Gly His Gln Asp Trp Leu Ser Gly Lys Gln	
420 425 430	
ttc aag tgc aaa gtc aac aac aaa gcc ctc cca tcc ccc att gag gag	1344
Phe Lys Cys Lys Val Asn Asn Lys Ala Leu Pro Ser Pro Ile Glu Glu	
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atc atc tcc aag acc cca ggg cag gcc cat cag cct aat gtg tat gtc	1392
Ile Ile Ser Lys Thr Pro Gly Gln Ala His Gln Pro Asn Val Tyr Val	
450 455 460	
ctg ccg cca tcg cgg gat gag atg agc aag aat acg gtc acc ctg acc	1440
Leu Pro Pro Ser Arg Asp Glu Met Ser Lys Asn Thr Val Thr Leu Thr	
465 470 475 480	
tgt ctg gtc aaa gac ttc ttc cca cct gag att gat gtg gag tgg cag	1488
Cys Leu Val Lys Asp Phe Phe Pro Pro Glu Ile Asp Val Glu Trp Gln	
485 490 495	
agc aat gga cag cag gag cct gag agc aag tac cgc atg acc ccg ccc	1536
Ser Asn Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg Met Thr Pro Pro	
500 505 510	
cag ctg gat gaa gat ggg tcc tac ttc cta tac agc aag ctc tcc gtg	1584
Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val	
515 520 525	
gac aag agc cgc tgg cag cgg gga gac acc ttc ata tgt gcg gtg atg	1632
Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile Cys Ala Val Met	
530 535 540	
cat gaa gct cta cac aac cac tac aca cag ata tcc ctc tcc cat tct	1680
His Glu Ala Leu His Asn His Tyr Thr Gln Ile Ser Leu Ser His Ser	
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ccg ggt aaa tga	1692
Pro Gly Lys	

<210> 78  
 <211> 563  
 <212> PRT

<213> Canis familiaris

<400> 78

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Phe	Glu	Ile	Val	Asp	Pro	Gly	Tyr	Leu	Gly	Tyr	Leu	Ser	Leu	Gln	Trp
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Gln	Pro	Pro	Leu	Phe	Pro	Asp	Asn	Phe	Lys	Glu	Cys	Thr	Ile	Glu	Tyr
		35					40					45			
Glu	Leu	Lys	Tyr	Arg	Asn	Ile	Asp	Ser	Glu	Asn	Trp	Lys	Thr	Ile	Ile
	50					55					60				
Thr	Lys	Asn	Leu	His	Tyr	Lys	Asp	Gly	Phe	Asp	Leu	Asn	Lys	Gly	Ile
65					70					75					80
Glu	Ala	Lys	Ile	Asn	Thr	Leu	Leu	Pro	Ala	Gln	Cys	Thr	Asn	Gly	Ser
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Glu	Val	Arg	Ser	Ser	Trp	Ala	Glu	Thr	Thr	Tyr	Trp	Thr	Ser	Pro	Gln
			100					105					110		
Gly	Asn	Arg	Glu	Thr	Lys	Ile	Gln	Asp	Met	Asp	Cys	Val	Tyr	Tyr	Asn
		115					120					125			
Trp	Gln	Tyr	Leu	Val	Cys	Ser	Trp	Lys	Pro	Gly	Met	Gly	Val	His	Phe
	130					135					140				
Asp	Thr	Asn	Tyr	Gln	Leu	Phe	Tyr	Trp	Tyr	Glu	Gly	Leu	Asp	His	Ser
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Ala	Glu	Cys	Thr	Asp	Tyr	Ile	Lys	Val	Asn	Gly	Lys	Asn	Met	Gly	Cys
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Arg	Phe	Pro	Tyr	Leu	Glu	Ser	Ser	Asp	Tyr	Lys	Asp	Phe	Tyr	Ile	Cys
			180					185					190		
Val	Asn	Gly	Ser	Ser	Glu	Ser	Gln	Pro	Ile	Arg	Pro	Ser	Tyr	Phe	Ile
		195					200					205			
Phe	Gln	Leu	Gln	Asn	Ile	Val	Lys	Pro	Met	Pro	Pro	Asp	Tyr	Leu	Ser
	210				215						220				
Leu	Thr	Val	Lys	Asn	Ser	Glu	Glu	Ile	Asn	Leu	Lys	Trp	Asn	Met	Pro
225					230					235				240	

Lys	Gly	Pro	Ile	Pro	Ala	Lys	Cys	Phe	Ile	Tyr	Glu	Ile	Glu	Phe	Thr	245	250	255
Glu	Asp	Gly	Thr	Thr	Trp	Val	Thr	Thr	Thr	Val	Glu	Asn	Glu	Ile	Gln	260	265	270
Ile	Thr	Arg	Thr	Ser	Asn	Glu	Ser	Gln	Lys	Leu	Cys	Phe	Leu	Val	Arg	275	280	285
Ser	Lys	Val	Asn	Ile	Tyr	Cys	Ser	Asp	Asp	Gly	Ile	Trp	Ser	Glu	Trp	290	295	300
Ser	Asp	Glu	Gln	Cys	Trp	Lys	Gly	Asp	Ile	Trp	Lys	Glu	Thr	Gly	Ser	305	310	315
Asn	Thr	Lys	Val	Asp	Lys	Pro	Val	Ala	Lys	Glu	Cys	Glu	Cys	Lys	Cys	325	330	335
Asn	Cys	Asn	Asn	Cys	Pro	Cys	Pro	Gly	Cys	Gly	Leu	Leu	Gly	Gly	Pro	340	345	350
Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Ile	Leu	Val	Thr	Ala	355	360	365
Arg	Thr	Pro	Thr	Val	Thr	Cys	Val	Val	Val	Asp	Leu	Asp	Pro	Glu	Asn	370	375	380
Pro	Glu	Val	Gln	Ile	Ser	Trp	Phe	Val	Asp	Ser	Lys	Gln	Val	Gln	Thr	385	390	395
Ala	Asn	Thr	Gln	Pro	Arg	Glu	Glu	Gln	Ser	Asn	Gly	Thr	Tyr	Arg	Val	405	410	415
Val	Ser	Val	Leu	Pro	Ile	Gly	His	Gln	Asp	Trp	Leu	Ser	Gly	Lys	Gln	420	425	430
Phe	Lys	Cys	Lys	Val	Asn	Asn	Lys	Ala	Leu	Pro	Ser	Pro	Ile	Glu	Glu	435	440	445
Ile	Ile	Ser	Lys	Thr	Pro	Gly	Gln	Ala	His	Gln	Pro	Asn	Val	Tyr	Val	450	455	460
Leu	Pro	Pro	Ser	Arg	Asp	Glu	Met	Ser	Lys	Asn	Thr	Val	Thr	Leu	Thr	465	470	475
Cys	Leu	Val	Lys	Asp	Phe	Phe	Pro	Pro	Glu	Ile	Asp	Val	Glu	Trp	Gln	485	490	495

Ser Asn Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg Met Thr Pro Pro  
500 505 510

Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val  
515 520 525

Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile Cys Ala Val Met  
530 535 540

His Glu Ala Leu His Asn His Tyr Thr Gln Ile Ser Leu Ser His Ser  
545 550 555 560

Pro Gly Lys

<210> 79

<211> 1692

<212> DNA

<213> Canis familiaris

<400> 79

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<211> 1686

<212> DNA

<213> Canis familiaris

<220>

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<400> 80

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ttt gag ata gtg gac cct gga tat tta ggt tat ctc tct ttg caa tgg 96  
Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp  
20 25 30

caa cct cca tta ttt ccg gat aat ttt aag gaa tgc aca ata gaa tat 144  
Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr  
35 40 45

gaa tta aaa tac cga aac att gat agt gaa aac tgg aag acc atc att 192  
Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile  
50 55 60

acc aag aat cta cat tac aaa gat ggg ttt gat ctt aac aaa ggt att 240  
Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile  
65 70 75 80

gaa gca aag ata aac aca ctt ctg cca gca caa tgc aca aat gga tca 288  
Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser  
85 90 95

gaa gtt aga agt tca tgg gca gaa act act tat tgg aca tca cca caa 336  
Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln  
100 105 110

gga aat cgg gaa act aaa att caa gat atg gac tgt gta tat tac aac 384  
Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn  
115 120 125



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Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe	
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gat acc aat tac cag ttg ttt tac tgg tat gag ggc ttg gac cat tca	480
Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser	
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gca gag tgt act gat tac atc aag gtt aat gga aaa aat atg gga tgc	528
Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys	
165 170 175	
agg ttt ccc tat ttg gag tca tca gac tat aaa gat ttc tac atc tgt	576
Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys	
180 185 190	
gtt aat ggg tca tca gaa tcc cag cct atc aga ccc agc tat ttt att	624
Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile	
195 200 205	
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Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser	
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ctt act gtg aag aat tca gag gaa att aac ctg aaa tgg aac atg cct	720
Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro	
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Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr	
245 250 255	
gag gat ggt act act tgg gtg act acc aca gtt gag aat gag ata caa	816
Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln	
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Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg	
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Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp	
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Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Gly Ser	
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ctc ccc att gag cac cag gac tgg ctc acc gga aag gag ttc aag tgc	1296
Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys	
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Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val Tyr Val Leu Pro Pro	
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Ile Lys Asp Phe Phe Pro Pro Glu Ile Asp Val Glu Trp Gln Ser Asn	
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gga cag ccg gag ccc gag agc aag tac cac acg act gcg ccc cag ctg	1536
Gly Gln Pro Glu Pro Glu Ser Lys Tyr His Thr Thr Ala Pro Gln Leu	
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 Ser Arg Trp Gln Gln Gly Asp Thr Phe Thr Cys Ala Val Met His Glu  
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gct cta cag aac cac tac aca gat cta tcc ctc tcc cat tct ccg ggt 1680  
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<210> 81  
 <211> 561  
 <212> PRT  
 <213> Canis familiaris

<400> 81  
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Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr  
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Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile  
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Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile  
 65 70 75 80

Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser  
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Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn  
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Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe  
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Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys			
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Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys			
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Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile			
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Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser			
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Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr			
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Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg			
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Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp			
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Asn Thr Lys Val Asp Lys Pro Val Pro Lys Glu Ser Thr Cys Lys Cys			
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Ile Ser Pro Cys Pro Val Pro Glu Ser Leu Gly Gly Pro Ser Val Phe			
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Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg Ile Thr Arg Thr Pro			
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Glu Ile Thr Cys Val Val Leu Asp Leu Gly Arg Glu Asp Pro Glu Val			
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Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val His Thr Ala Lys Thr			
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Gln Pro Arg Glu Gln Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val  
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Arg Val Asn His Ile Gly Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser  
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Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val Tyr Val Leu Pro Pro  
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Ser Pro Lys Glu Leu Ser Ser Ser Asp Thr Val Thr Leu Thr Cys Leu  
 465 470 475 480

Ile Lys Asp Phe Phe Pro Pro Glu Ile Asp Val Glu Trp Gln Ser Asn  
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Gly Gln Pro Glu Pro Glu Ser Lys Tyr His Thr Thr Ala Pro Gln Leu  
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Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys  
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Ala Leu Gln Asn His Tyr Thr Asp Leu Ser Leu Ser His Ser Pro Gly  
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Lys

<210> 82

<211> 1686

<212> DNA

<213> Canis familiaris

<400> 82

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gataggctgg gattctgatg acccattaac acagatgtag aaatctttat agtctgatga 1140
ctccaaatag ggaaacctgc atcccatatt ttttccatta accttgatgt aatcagtaca 1200
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gacacccatg ccagggtttcc aagagcagac taaatattgc cagttgtaat atacacagtc 1320
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ggtcttccag ttttactat caatgtttcg gtattttaat tcatattcta ttgtgcattc 1560
cttaaaatta tccggaaata atggagggtt ccattgcaaa gagagataac ctaaatatcc 1620
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agacat 1686

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<210> 83

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<220>

<221> misc\_feature

<222> (9)

<223> At position 9, n = unknown

<220>

<221> misc\_feature

<222> (18)

<223> At position 18, n = unknown

<220>

<221> misc\_feature

<222> (21)

<223> At position 21, n = unknown

<220>  
<221> misc\_feature  
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<223> At position 27, n = unknown

<400> 83  
athtggacnt ggaayccncc ngarggngc

29

<210> 84  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<220>  
<221> misc\_feature  
<222> (6)  
<223> At position 6, n = unknown

<220>  
<221> misc\_feature  
<222> (9)  
<223> At position 9, n = unknown

<220>  
<221> misc\_feature  
<222> (21)  
<223> At position 21, n = unknown

<220>  
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<222> (33)  
<223> At position 33, n = unknown

<400> 84  
atyttncng crtttrtcytt naccatdaty tgnac

35

<210> 85  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<220>  
<221> misc\_feature  
<222> (12)  
<223> At position 12, n = unknown

<220>  
<221> misc\_feature  
<222> (18)  
<223> At position 18, n = unknown

<220>  
<221> misc\_feature  
<222> (21)  
<223> At position 21, n = unknown

<400> 85  
garathaarg tnaayccncc ncargaytty garat

35

<210> 86  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<220>  
<221> misc\_feature  
<222> (12)  
<223> At position 12, n = unknown

<220>  
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<223> At position 22, n = unknown

<220>  
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<223> At position 31, n = unknown

<400> 86



<210> 87  
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 Primer

<220>  
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 <223> At position 7, n = unknown

<220>  
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 <223> At position 16, n = unknown

<220>  
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 <223> At position 25, n = unknown

<220>  
 <221> misc\_feature  
 <222> (40)  
 <223> At position 40, n = unknown

<400> 87  
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<210> 88  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 Primer

<220>  
 <221> misc\_feature  
 <222> (9)

<223> At position 9, n = unknown

<220>

<221> misc\_feature

<222> (12)

<223> At position 12, n = unknown

<400> 88

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23

<210> 89

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 89

agcggatccc tctatgcttt caaatgctga gataaaagtt aatcctcctc agg

53

<210> 90

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 90

tggacatcac cacaaggaaa tcggg

25

<210> 91

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 91

gcacatatgt ctatgctttc aaatgctgaa taaaagttaa tcctcctcag g

51

<210> 92  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 92  
aaaggatccg gtttccttcc agatattcatt tccagc 36

<210> 93  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 93  
ccgggatcca acactaaagt agacaagcgt g 31

<210> 94  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 94  
gcgctcgagt catttaccg gagaatggga ggg 33

<210> 95  
<211> 1525  
<212> DNA  
<213> Canis familiaris

<400> 95  
gaattcggca cgaggagag gaggagggaa agatagaaag agagagagaa agattgcttg 60

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aaacagtaga	gattcaat	agtgtcta	gtggaaagga	ggacaaagag	gtcttgtgat	180
aactgcctgt	gataatacat	ttcttgagaa	accatattat	tgagtagagc	tttcagcaca	240
ctaaatcctg	gagaaatggc	ttttgtgcat	atcagatgct	tgtgtttcat	tcttctttgt	300
acaataactg	gctattcttt	ggagataaaa	gttaatcctc	ctcaggattt	tgaaatattg	360
gatectggat	tacttgggta	tctctatttg	caatggaaac	ctcctgtggg	tatagaaaaa	420
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gaaggaaaga	tacgtacgca	tttgtcagag	cattgtacaa	atggatcaga	agtacaaagt	600
ccatggatag	aagcttctta	tgggatatca	gatgaaggaa	gtttggaaac	taaaattcag	660
gacatgaagt	gtatatatta	taactggcag	tatttgggtc	gctcttgga	acctggcaag	720
acagtatatt	ctgataccaa	ctataccatg	ttttcttggg	atgagggtt	ggatcatgcc	780
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ttggactcat	cagactataa	agattttttt	atctgtgtta	atggatcttc	aaagttggaa	900
cccatcagat	ccagctatac	agtttttcaa	cttcaaaata	tagttaaacc	attgccacca	960
gaattccttc	atattagtgt	ggagaattcc	attgatatta	gaatgaaatg	gagcacacct	1020
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attttcatag	taccagtttg	tcttttcttt	atattccttt	tgttacttct	ttgccttatt	1320
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tgtgcttatg	aagataccct	ctgttaaacc	accaatttct	tgacatagag	ccagccagca	1440
ggagtcatat	taaactcaat	ttctcttaaa	atttcgaata	catcttcttg	aaaatccaaa	1500
aaaaaaaaaa	aaaaaaaaac	tcgag				1525

<210> 96

<211> 1369

<212> DNA

<213> Canis familiaris

<400> 96

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ggcggggaga	gaggcaatat	caaggtttta	aatctcggag	aaatggcttt	cgtttgcttg	120
gctatcggat	gcttatatac	ctttctgata	agcacaacat	ttggctgtac	ttcatcttca	180
gacaccgaga	taaaagttaa	ccctcctcag	gattttgaga	tagtggatcc	cggatactta	240
ggttatctct	atttgcaatg	gcaaccccca	ctgtctctgg	atcattttta	ggaatgcaca	300
gtggaatatg	aactaaaata	ccgaaacatt	ggtagtgaag	catggaagac	catcattact	360
aagaatctac	attacaaaga	tgggtttgat	cttaacaagg	gcattgaagc	gaagatacac	420
acgctttttac	catggcaatg	cacaaatgga	tcagaagttc	aaagttcctg	ggcagaaact	480
acttattgga	tatcaccaca	aggaattcca	gaaactaaag	ttcaggatat	ggattgcgta	540
tattacaatt	ggcaatat	actctgttct	tggaaacctg	gcataggtgt	acttcttgat	600
accaattaca	acttgtttta	ctgggatgag	ggcttggatc	atgcattaca	gtgtgttgat	660
tacatcaagg	ctgatggaca	aaatatagga	tgagatttct	cctatttgga	ggcatcagac	720
tataaagatt	tctatatttg	tgttaatgga	tcatacagaga	acaagcctat	cagatccagt	780
tatttcactt	ttcagcttca	aaatatagtt	aaacctttgc	cgccagtcta	tcttactttt	840
actcgggaga	gttcatgtga	aattaagctg	aaatggagca	tacctttggg	acctattcca	900

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gtagtaagaa gcaaagtga tattttattgc tcagatgacg gaatttggag tgagtggagt 1080  
gataaacaat gctgggaagg tgaagacctt tcgaagaaaa ctttgctacg tttctggcta 1140  
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aacacctacc caaaaatgat tccagaattt ttctgtgata catgaagact ttccatatca 1260  
agagacatgg tattgactca acagtttcca gtcattggcca aatgttcaat atgagtctca 1320  
ataaactgaa tttttcttgc gaaaaaaaaa aaaaaaatc cgcggatcc 1369

<210> 97

<211> 1525

<212> DNA

<213> *Canis familiaris*

<400> 97

ctcgagtttt tttttttttt ttttttttgg attttcaaga agatgtattc gaaattttta 60  
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aacagagggg atcttcataa gcacacactt ctttgctcag atccacatgg aggtcctaat 180  
tggtgtcagg ttcttccttc tccacaataa ggcaaagaag taacaaaagg aatataaaga 240  
aaagacaaac tgggtactatg aaaataatct ttgagtctgg ccctgtgtaa ccttcccaac 300  
attcctcttc actccattcg ctccaaattc catcatctgc acaatatata ttgaccttac 360  
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ttttgtctgt ggcagactcc caggaaatat cgtcttctcg gatcacaatt tcataagtgt 480  
aacaccttgg tggaatgggt cctccagggt tgctccattt cattctaata tcaatggaat 540  
tctccacact aatatgaagg aattctggtg gcaatgggtt aactatattt tgaagttgaa 600  
aaactgtata gctggatctg atgggttcca actttgaaga tccattaaca cagataaaaa 660  
aatctttata gtctgatgag tccaagttgg acagtttgca tccaacattt ttttcatcat 720  
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caaaagccat ttctccagga tttagtgtgc tgaaagctct actcaataat atggtttctc 1320  
aagaaatgta ttatcacagg cagttatcac aagacctctt tgtcctcctt tccacattag 1380  
acactaaatt gaatctctac tgttttcctt ccttatacgt gaagagcaaa gcactgtctt 1440  
gagagaggtc actgttcagg ggtagcaagc aatctttctc tctctcttcc tatctttccc 1500  
tcctcctctc cctcgtgccg aattc 1525

<210> 98

<211> 1369

<212> DNA

<213> *Canis familiaris*

<400> 98  
ggatccgcgg atttttttttt ttttttttcg caagaaaaat tcagtttatt gagactcata 60  
ttgaacattt ggccatgact ggaaactgtt gagtcaatac catgtctctt gatatggaaa 120  
gtcttcatgt atcacagaaa aattctggaa tcatttttgg gtaggtgttt ggcttacgca 180  
aaagcagacc ggttacaaat ataactaata ttaagatgaa accaaatggg agccagaaac 240  
gtagcaaagt tttcttcgat aggtcttcac cttcccagca ttgtttatca ctccactcac 300  
tccaaattcc gtcactctgag caataaatat tcaacttgct tcttactaca aagcataatt 360  
gtcgggtttc atttgttggt ttcaagggtg atgtttcatt ttcaactgta gcagtcacca 420  
aggtagtata atcttctctg atctcaattt cataatcaaa acaccttgct ggaatagggtc 480  
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agactggcgg caaagggttta actatatattt gaagctgaaa agtgaaataa ctggatctga 600  
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gtaatgcatg atccaagccc tcataccagt aaaacaagtt gtaattggta tcaagaagta 780  
cacctatgcc aggtttccaa gaacagagta aatattgcca attgtaatat acgcaatcca 840  
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aagccatttc tccgagattt aaaaccttga tattgcctct ctccccgccg acaggcacac 1320  
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<210> 99

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 99

ctctactatt ggcacagcag cctggga 27

<210> 100

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 100  
agtcagagca aaggaacaac caatgtg 27

<210> 101  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 101  
cctcccgagg gagccagccc g 21

<210> 102  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 102  
cgggctggct ccctcgggag g 21

<210> 103  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 103  
catggtcccc ggcgttcttc c 21

<210> 104  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 104

ggtgagaata ccgacccac g

21